

## SEQUENCE LISTING

<110> Genentech, Inc.  
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<120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

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<140> 09/665,350  
<141> 2000-09-18

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 Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr  
 35 40 45  
 Ala Lys Lys Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr  
 50 55 60  
 Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu  
 65 70 75 80  
 Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala  
 85 90 95  
 Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr  
 100 105 110  
 Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys  
 115 120 125  
 Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser  
 130 135 140

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg  
 145 150 155 160  
 Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
 165 170 175  
 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
 180 185 190  
 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
 195 200 205  
 Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
 210 215 220  
 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
 225 230 235 240  
 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
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 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
 260 265 270  
 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
 275 280 285  
 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
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 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
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aacagccctg gctgaggggag ctgcagcgca gcagagtatac tgacggcgcc aggttgcgta 180
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<210> 4

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<212> PRT

<213> Homo sapiens

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20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

65	70	75	80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln			
85	90	95	
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly			
100	105	110	
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro			
115	120	125	
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln			
130	135	140	
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu			
145	150	155	160
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr			
165	170	175	
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Phe Cys			
180	185	190	
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His			
195	200	205	
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys			
210	215	220	
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn			
225	230	235	240
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys			
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Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln			
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Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys			
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Ile Gly Lys Ser Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu			
290	295	300	
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys			
305	310	315	320
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His			
325	330	335	
Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala			
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<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
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<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 7  
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<220>  
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oligonucleotide probe

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<210> 9  
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<220>  
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 oligonucleotide probe

<400> 9  
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<210> 10  
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<210> 11  
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 ctactgctgt tgctgcccgtt ggctggccac ttggctctgg gtgcccagca gggtcgtggg 180  
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<212> PRT  
<213> Homo sapiens

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Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys  
35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu  
50 55 60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr  
65 70 75 80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro  
85 90 95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr  
100 105 110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln  
115 120 125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln  
130 135 140

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly  
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His Asp Pro Gly

<210> 13  
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 <223> a, t, c or g

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 <222> (80)  
 <223> a, t, c or g

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 <223> a, t, c or g

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 <223> a, t, c or g

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 <223> Description of Artificial Sequence: Synthetic  
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Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
 180 185

&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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tgcttgcta ctcctgcaaa gccc

24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 20  
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<210> 21  
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<210> 22  
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<212> DNA  
<213> Homo sapiens

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gaccgaccag ctgagcaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180  
caagcacgtg caggtcacccg ggcgtcgcat ctccgccccacc gcccggggacg gcaacaagtt 240  
tgccaagctc atagtggaga cggacacgtt tggcagccgg gttcgcata aaggggctga 300  
gagtggaaag tacatctgtt tgaacaagag gggcaagctc atcgggaagc ccagcgggaa 360  
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gacgggtggc aggcccttggg gaggaactga gtgtcacccct gatctcaggc caccagcctc 900  
tgccgcctc ccagccgggc tcctgaagcc cgctgaaagg tcagcgactg aaggccctgc 960  
agacaaccgt ctggagggtgg ctgtcctcaa aatctgcttc tcggatctcc ctcagtcgc 1020  
ccccagcccc caaactcctc ctggcttagac tgttaggaagg gactttgtt tggttccactc 1080  
tttcaggaaa aaagaaaagg agagagagga aaatagaggg ttgttccactc ctcacattcc 1140  
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<210> 23  
<211> 205  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 23

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Leu	Ile	Leu	Cys	Cys	Gln	Thr	Gln	Tyr	Val	Arg	Asp	Gln	Gly	Ala	Met
					20			25					30		

Thr	Asp	Gln	Leu	Ser	Arg	Arg	Gln	Ile	Arg	Glu	Tyr	Gln	Leu	Tyr	Ser
					35			40				45			

Arg	Thr	Ser	Gly	Lys	His	Val	Gln	Val	Thr	Gly	Arg	Arg	Ile	Ser	Ala
					50			55				60			

Thr	Ala	Glu	Asp	Gly	Asn	Lys	Phe	Ala	Lys	Leu	Ile	Val	Glu	Thr	Asp
					65			70			75		80		

Thr	Phe	Gly	Ser	Arg	Val	Arg	Ile	Lys	Gly	Ala	Glu	Ser	Glu	Lys	Tyr
					85			90			95				

Ile	Cys	Met	Asn	Lys	Arg	Gly	Lys	Leu	Ile	Gly	Lys	Pro	Ser	Gly	Lys
					100			105			110				

Ser	Lys	Asp	Cys	Val	Phe	Thr	Glu	Ile	Val	Leu	Glu	Asn	Asn	Tyr	Thr
					115			120			125				

Ala	Phe	Gln	Asn	Ala	Arg	His	Glu	Gly	Trp	Phe	Met	Ala	Phe	Thr	Arg
					130			135			140				

Gln	Gly	Arg	Pro	Arg	Gln	Ala	Ser	Arg	Ser	Arg	Gln	Asn	Gln	Arg	Glu
					145			150			155		160		

Ala	His	Phe	Ile	Lys	Arg	Leu	Tyr	Gln	Gly	Gln	Leu	Pro	Phe	Pro	Asn
					165			170			175				

His	Ala	Glu	Lys	Gln	Lys	Gln	Phe	Glu	Phe	Val	Gly	Ser	Ala	Pro	Thr
					180			185			190				

Arg	Arg	Thr	Lys	Arg	Thr	Arg	Arg	Pro	Gln	Pro	Leu	Thr			
					195			200			205				

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

28

&lt;210&gt; 25

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 25
ccggtgacct gcacgtgctt gccca 24

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<220>
<221> modified_base
<222> (21)
<223> a, t, c or g

<400> 26
gcggatctgc cgccctgctca nctggtcggc catggcgccc t 41

<210> 27
<211> 2479
<212> DNA
<213> Homo sapiens

<400> 27
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ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180
tccagtccatt ttgatttgc tggttatttt tttttcttt ttcttttcc caccacattg 240
tattttattt ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300
ctttttccct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360
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tctacctgtt tgcaacccaa ctggacgaat tccccatgaa ctttcccaag aatgtcagag 600
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tgaagcttga agagctgcac ctggatgaca actccatata cacagtgggg gtgaaagacg 720
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atctgatcag gctctattt caggacaacc agataaaacca cattcctttt acagccttct 1080
caaattcqcg taaqctqqaa cqgctqqata tatccaacaa ccaactgcgg atgctgactc 1140
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 ccaccatgc ctccatctg aacaacggca gcaacacaggc gtccagccat gagcagacga 1860  
 cgtccacacag catgggctcc cccttctgc tggcggtt gatcgggggc gcggtgatata 1920  
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 tgggatttaa aaaaagtgt atctttcta ttcaagttt attacaaaca gttttgttaac 2460  
 tcttgcttt ttaatctt 2479

&lt;210&gt; 28

&lt;211&gt; 660

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu

1

5

10

15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys  
20 25 30Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr  
35 40 45Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly  
50 55 60Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe  
65 70 75 80Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr  
85 90 95Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg  
100 105 110Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala  
115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140  
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300  
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

405	410	415
Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val		
420	425	430
Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met		
435	440	445
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly		
450	455	460
Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu		
465	470	475
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu		
485	490	495
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala		
500	505	510
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser		
515	520	525
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala		
530	535	540
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser		
545	550	555
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys		
565	570	575
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly		
580	585	590
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln		
595	600	605
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu		
610	615	620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His		
625	630	635
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu		
645	650	655
His Cys His Thr		
660		
<210> 29		
<211> 21		
<212> DNA		

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 29  
cggtctacct gtatggcaac c 21

<210> 30  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 30  
gcaggacaac cagataaacc ac 22

<210> 31  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 31  
acgcagattt gagaaggctg tc 22

<210> 32  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 32  
ttcacgggct gctttgcc agctttgaa gcttgaagag ctgcac 46

<210> 33  
<211> 3449  
<212> DNA  
<213> Homo sapiens

<400> 33  
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cggtggctg cggccctgcc tcgcttcccc ggcgcggcg gtcgcggct 180  
tgcccctctt gctgcgcctt aaaatggaaa agatgctcg aggctgttt ctgctgatcc 240  
tcggacagat cgtccctcctc cctgcccagg ccagggagcg gtcacgtggg aggtccatct 300  
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<210> 34  
 <211> 915  
 <212> PRT  
 <213> Homo sapiens

<400> 34															
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				20				25					30		
Ser	Arg	Gly	Arg	His	Ala	Arg	Thr	His	Pro	Gln	Thr	Ala	Leu	Leu	Glu
	35					40							45		
Ser	Ser	Cys	Glu	Asn	Lys	Arg	Ala	Asp	Leu	Val	Phe	Ile	Ile	Asp	Ser
	50				55					60					
Ser	Arg	Ser	Val	Asn	Thr	His	Asp	Tyr	Ala	Lys	Val	Lys	Glu	Phe	Ile
	65				70				75					80	
Val	Asp	Ile	Leu	Gln	Phe	Leu	Asp	Ile	Gly	Pro	Asp	Val	Thr	Arg	Val
				85				90					95		
Gly	Leu	Leu	Gln	Tyr	Gly	Ser	Thr	Val	Lys	Asn	Glu	Phe	Ser	Leu	Lys
				100				105					110		
Thr	Phe	Lys	Arg	Lys	Ser	Glu	Val	Glu	Arg	Ala	Val	Lys	Arg	Met	Arg
	115					120						125			
His	Leu	Ser	Thr	Gly	Thr	Met	Thr	Gly	Leu	Ala	Ile	Gln	Tyr	Ala	Leu
	130				135						140				
Asn	Ile	Ala	Phe	Ser	Glu	Ala	Glu	Gly	Ala	Arg	Pro	Leu	Arg	Glu	Asn
	145				150				155				160		
Val	Pro	Arg	Val	Ile	Met	Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Ser
				165				170					175		
Val	Ala	Glu	Val	Ala	Ala	Lys	Ala	Arg	Asp	Thr	Gly	Ile	Leu	Ile	Phe
				180				185					190		
Ala	Ile	Gly	Val	Gly	Gln	Val	Asp	Phe	Asn	Thr	Leu	Lys	Ser	Ile	Gly
	195					200						205			
Ser	Glu	Pro	His	Glu	Asp	His	Val	Phe	Leu	Val	Ala	Asn	Phe	Ser	Gln
	210				215						220				
Ile	Glu	Thr	Leu	Thr	Ser	Val	Phe	Gln	Lys	Lys	Leu	Cys	Thr	Ala	His

225	230	235	240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile			
245		250	255
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser			
260		265	270
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His			
275		280	285
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln			
290		295	300
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala			
305		310	315
Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val			
325		330	335
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu			
340		345	350
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn			
355		360	365
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr			
370		375	380
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys			
385		390	395
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu			
405		410	415
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe			
420		425	430
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu			
435		440	445
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser			
450		455	460
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys			
465		470	475
480			
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu			
485		490	495
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu			
500		505	510

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
 515 520 525  
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp  
 530 535 540  
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp  
 545 550 555 560  
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly  
 565 570 575  
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys  
 580 585 590  
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys  
 595 600 605  
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser  
 610 615 620  
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile  
 625 630 635 640  
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu  
 645 650 655  
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn  
 660 665 670  
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly  
 675 680 685  
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser  
 690 695 700  
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg  
 705 710 715 720  
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu  
 725 730 735  
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly  
 740 745 750  
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro  
 755 760 765  
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu  
 770 775 780  
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser  
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
 805 810 815  
 Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
 820 825 830  
 Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
 835 840 845  
 Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
 850 855 860  
 Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
 865 870 875 880  
 Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
 885 890 895  
 Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
 900 905 910  
 Arg Tyr Arg  
 915

<210> 35  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 35  
 gtgaccctgg ttgtgaatac tcc 23

<210> 36  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 36  
 acagccatgg tctatagctt gg 22

<210> 37  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 37  
gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag 45

<210> 38  
<211> 1813  
<212> DNA  
<213> Homo sapiens

<400> 38  
ggagccgccc tgggtgtcag cggctcggt cccgcgcacg ctccggccgt cgccgcagcct 60  
ccgcacacctc aggtccgtgc gtccccggc tggcgccct gactccgtcc cggccaggaa 120  
ggccatgt ttccctcccg gggcccttgg tgaccacatt gctgcgggtt ttgtccctgg 180  
ggctgagtgc ctcgcgcgc ccctcgccgg cccagctgca actgcacttg cccgccaacc 240  
ggttgcaggc ggtggaggaa gggaaagtgg tgcttccagc gtggtaacacc ttgcacgggg 300  
aggtgtcttc atcccagcca tgggaggtgc ctttgcgtat gtgggtcttc aaacagaaag 360  
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ccttggctca ctccatgccc tcccgaaacc tgccctgcg gctggagggt ctccaggaga 480  
aagactctgg cccctacagc tgctccgtga atgtgcaga caaacaaggc aaatcttaggg 540  
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gtctccaggc tggcccccgt gtgggggcaa acgtgacccct gagtgcacgg tctccaaggaa 660  
gtaagccgc tggccaaatac cagtgggatc ggcagcttcc atccctccag actttcttg 720  
caccagcatt agatgtcatc cgtgggtctt taagcctcac caaccttcg tcttccatgg 780  
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aggagccagc caatgataatc aaggaggatg ccattgcctcc ccggaccctgc ccctggccca 1020  
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accatctcag taagaccaa gtgtccagga gacagaaggaa gaagaggaaatggatctggaa 1500  
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taaaactaac atgaaatatg tgggttttc atttgcataat ttaaataaaatg atacataatg 1800  
tttgcataatgaaa 1813

<210> 39  
<211> 390  
<212> PRT  
<213> Homo sapiens

<400> 39  
Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

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Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln			
20	25	30	
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val			
35	40	45	
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln			
50	55	60	
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys			
65	70	75	80
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro			
85	90	95	
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg			
100	105	110	
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val			
115	120	125	
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr			
130	135	140	
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu			
145	150	155	160
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser			
165	170	175	
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro			
180	185	190	
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser			
195	200	205	
Leu Ser Leu Thr Asn Leu Ser Ser Met Ala Gly Val Tyr Val Cys			
210	215	220	
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu			
225	230	235	240
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly			
245	250	255	
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His			
260	265	270	
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp			
275	280	285	

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
                   340                  345                  350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
370 375 380

Gln Ala Gly Ser Leu Val  
385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> De

oligonucleotide probe

aqqgtctc

<211> 24

<212> DN

<213> Art

(215) *Thomomys* sp. sp.

223

**oligonucleotide probe**

attatggc

acccggggcc ccggggatcc cgtt

<211> 50

<211> 50

-213- Art

<213> Artificial Sequence

220

<2223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 42		
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc		50
<210> 43		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 43		
gtgtgacaca gcgtgggc		18
<210> 44		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 44		
gaccggcagg cttctgcg		18
<210> 45		
<211> 25		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 45		
cagcagattc agccaccagg agtgg		25
<210> 46		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 46		
ctgagccgtg ggctgcagtc tcgc		24
<210> 47		

<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 47  
 ccgactacga ctggttttc atcatgcagg atgacacata tgtgc 45

<210> 48  
 <211> 2822  
 <212> DNA  
 <213> Homo sapiens

<400> 48  
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 gtggaaatacg caatggaaatt gaaggcctgct attgcaacat gggattttca ggaaatggtg 180  
 tcacaattttt tgaagatgtt aatgaatgtt gaaatttaac tcagtcctgt ggccggaaatg 240  
 ctaattgcac taacacagaaa ggaagtttattt attgtatgtt tgtagcttgc ttccatggcc 300  
 gcagtaacca agacagggtt atcactaatg atggaaccgtt ctgtatagaa aatgtgaatg 360  
 ccaaactgcca ttttagataat gtctgtatag ctgcaaatat taataaaaaact ttaacaaaaaa 420  
 tcagatccat aaaagaacctt gtggcttgc tacaagaagt ctatagaaat tctgtgacag 480  
 atctttcacc aacagatata attacatata tagaaatattt agctgaatca tcttcattttc 540  
 taggttacaa gaacaacact atctcagccca aggacaccctt ttctactca actcttactg 600  
 aattttgtaaa aaccgtgaat aattttgttc aaagggtatc attttgttagt tgggacaagt 660  
 tatctgtgaa tcatagggaaa acacatcttta caaaaactcat gcacactgtt gaacaagcta 720  
 cttaaggat atcccagagc ttccaaaaga ccacaggtt tgatacaat tcaacggata 780  
 tagctctcaa agttttcttt tttgattcat ataacatgaa acatattcat cctctatga 840  
 atatggatgg agactacata aatatatttc caaagagaaaa agctgcataat gattcaatg 900  
 gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgtt tcatcatctg 960  
 acaacttctt attgaaacactt caaaaattatg ataattctga agaggaggaa agagtcatat 1020  
 cttagtaat ttctgttca atgagcttca acccaccac atttatgaa cttggaaaaaa 1080  
 taacatttac attaagtcat cggaaaggatca cagataggta taggagtctt tggatgtt 1140  
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 gaatgaactg tttttctgt agactagctg agaaaattttt gacataaaaat aaagaattta 2640  
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 agacttctgt ttgctaaatc tgtttcttt tctaataatc taaaaaaaaaaa aaaaaggttt 2760  
 acctccacaa attgaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2820  
 aa 2822

<210> 49  
<211> 690  
<212> PRT  
<213> Homo sapiens

<400> 49  
Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys  
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Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys  
20 25 30

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe  
35 40 45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn  
50 55 60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly  
65 70 75 80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln  
85 90 95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn  
100 105 110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys  
115 120 125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln  
130 135 140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile  
145 150 155 160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys  
165 170 175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

180	185	190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val		
195	200	205
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys		
210	215	220
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe		
225	230	235
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys		
245	250	255
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met		
260	265	270
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala		
275	280	285
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser		
290	295	300
Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln		
305	310	315
Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile		
325	330	335
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys		
340	345	350
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser		
355	360	365
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp		
370	375	380
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser		
385	390	395
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly		
405	410	415
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln		
420	425	430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr		
435	440	445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys		
450	455	460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly  
 465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu  
 485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly  
 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe  
 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val  
 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys  
 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly  
 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile  
 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser  
 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu  
 610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His  
 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln  
 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln  
 660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys  
 675 680 685

Leu Arg  
 690

<210> 50  
 <211> 589  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (61)

<223> a, t, c or g

<400> 50

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 gtattggtcc ct当地gatc aacttcttat tgaaacctca aaattatgat 180  
 aattctgaag aggaggaaag agtcatact tc当地taattt cagtc当地at gagctcaa 240  
 ccaccacat tatataact tgaaaaata acatttacat taagtc当地cg aaaggcaca 300  
 gataggata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360  
 tggcttc当地 agggctgtga gctgacatac tcaaattgaga cccacacctc atgccgctgt 420  
 aatcacctga cacatttgc aattttgatg tc当地ctggc cttccattgg tattaaagat 480  
 tataatattc ttacaaggat cactcaacta ggaataatta tttcaactgat ttgtcttgcc 540  
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<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 52

ggagtagaaaa gcgcatgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 54		
cgagctcgaa ttaattcg	18	
<210> 55		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 55		
ggatctcctg agctcagg	18	
<210> 56		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 56		
cctagttgag tgatccttgt aag	23	
<210> 57		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 57		
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<210> 58		
<211> 2137		
<212> DNA		
<213> Homo sapiens		
<400> 58		
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 tgctcggtg tcttggcac ctaccgtgg ggcccgttaag gcgctactat ataaggctgc 300  
 cggcccccggag ccgcgcgcgc gtcagagcag gagcgctgcg tccaggatct agggccacga 360  
 ccatcccaac cggcactca cagccccca gecatccccg gtcgcgcgcg agectccgc 420  
 accccccatcg cggagactgc gccgagagcc ccagggaggtt gccatgcggg gcggtgtgt 480  
 ggtggtccac gtatggatcc tggccggctt ctggctggcc gtggccggc gccccctcgc 540  
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 gaacccttcc cccagcactt ggtttccaa catgatattt atgagtaatt tattttgata 2040  
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<210> 59  
 <211> 216  
 <212> PRT  
 <213> Homo sapiens

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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
 50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65                   70                   75                   80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85                   90                   95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100               105               110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115               120               125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130               135               140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145               150               155               160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165               170               175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180               185               190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195               200               205

Val Arg Ser Pro Ser Phe Glu Lys  
 210               215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgtta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 61

gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta

42

<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 62  
 ccagtccgtt gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
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 gtcgtctgt cgctacctgg tggtcgcctt gggctatcat aaggctatg gttttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtagccaa gaggctattt tagcctgcaa 240  
 aaccccaaag aagactgttt cctccagatt agagtgaaag aaactgggtc ggagtgtctc 300  
 ctttgtctac tatcaacaga ctcttcaagg tgatttaaa aatcgagctg agatgataga 360  
 tttaataatc cgatcaaaa atgtgacaag aagtgtatgcg gggaaatatc gttgtgaagt 420  
 tagtgcggccca tctgagcaag gccaaacctt ggaagaggat acagtcactc tggaaagtatt 480  
 agtggctcca gcagttccat catgtgaagt acccttttgc gctctgagtg gaactgtgt 540  
 agagctacga tgtcaagaca aagaaggaa tccagctctt gaatacacat gttttaaagga 600  
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 acccgggagg cgaggttgc agttagctga gatcacgcca ctgcagttcc gcctggtaa 1200  
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 tgtagaattt ttacaataaa tatacggtt tattc 1295

<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
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 1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
     35                        40                        45

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
     50                        55                        60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
     65                        70                        75                        80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
     85                        90                        95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
     100                       105                       110

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
     115                       120                       125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
     130                       135                       140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
     145                       150                       155                       160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
     165                       170                       175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
     180                       185                       190

Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
     195                       200                       205

Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
     210                       215                       220

Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
     225                       230                       235                       240

Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
     245                       250                       255

Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
     260                       265                       270

Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
     275                       280                       285

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
     290                       295                       300

Gly Gly Ser Arg Gly Gln Glu Phe

305	310	
<pre> &lt;210&gt; 65 &lt;211&gt; 22 &lt;212&gt; DNA &lt;213&gt; Artificial Sequence </pre>		
<pre> &lt;220&gt; &lt;223&gt; Description of Artificial Sequence: Synthetic       oligonucleotide probe </pre>		
<pre> &lt;400&gt; 65 atcggttga agtttagtgcc cc </pre>		
22		
<pre> &lt;210&gt; 66 &lt;211&gt; 23 &lt;212&gt; DNA &lt;213&gt; Artificial Sequence </pre>		
<pre> &lt;220&gt; &lt;223&gt; Description of Artificial Sequence: Synthetic       oligonucleotide probe </pre>		
<pre> &lt;400&gt; 66 acctgcgata tccaacagaaa ttg </pre>		
23		
<pre> &lt;210&gt; 67 &lt;211&gt; 48 &lt;212&gt; DNA &lt;213&gt; Artificial Sequence </pre>		
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48		
<pre> &lt;210&gt; 68 &lt;211&gt; 2639 &lt;212&gt; DNA &lt;213&gt; Homo sapiens </pre>		
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<210> 69  
 <211> 708  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
 Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile  
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Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu  
 20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met  
 35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro  
 50 55 60

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Gln Thr Asn Asn  
 65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
 180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile  
 260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala  
 290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
 305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

Asn	Thr	Thr	Thr	Leu	Met	Ala	Cys	Leu	Gly	Gly	Leu	Leu	Gly	Ile	Ile
625					630					635					640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
           660                   665                   670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

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<210> 70  
<211> 1305  
<212> DNA  
<213> Homo sapiens
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<210> 71  
<211> 259  
<212> PRT  
<213> *Homo sapiens*

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu  
 1 5 10 15

Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser  
 20 25 30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val  
 35 40 45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
 65 70 75 80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
 130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met  
 145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val  
 165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala  
 180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val  
 195 200 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
 210 215 220

Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
 225 230 235 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser  
 245 250 255

Thr Val Val

&lt;210&gt; 72

&lt;211&gt; 2290

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

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 aaaaaaaaaa 2290

&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro

1

5

10

15

- 0 4 2 6 8 0 6 0 5 0

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly  
 20 25 30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys  
 35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
 50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
 65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
 85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro  
 100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser  
 115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn  
 130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp  
 145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp  
 165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser  
 180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
 195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
 210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
 225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
 245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
 260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
 275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320

Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335

Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445

Asp Gly Asp Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr  
 530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu  
 565 570 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590
Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser		
595	600	605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile	
610	615

<210> 74  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 74  
tcacctggag cctttattgg cc

22

<210> 75  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 75  
ataccagcta taaccaggct gcg

23

<210> 76  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 76  
caacagtaag tggtttgatg ctcttccaaa tcttagagatt ctgatgattg  
gg

50

52

<210> 77  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 77 ccatgtgtct ctcctacaa ag	22
<210> 78 <211> 23 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 78 gggaatagat gtgatctgat tgg	23
<210> 79 <211> 50 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 79 cacctgttagc aatgcaaattc tcaaggaaat acctagagat cttccctcctg	50
<210> 80 <211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 80 agcaaccgccc tgaagctcat cc	22
<210> 81 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 81 aaggcgcggt gaaaatgtt gacg	24
<210> 82	

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 82  
 gactacatgt ttcaggacct gtacaacctc aagtcaactgg aggttggcga 50

<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
 cccacgcgtc cgcacctcg ccgggggtc cgaagcggt cggggggcgcc ctttcggtca 60  
 acatcgtagt ccacccccc cccatccccca gccccccgggg attcaggctc gccagcgccc 120  
 agccaggggag ccggccggga agcgcgatgg gggccccagc cgcctcgctc ctgctcctgc 180  
 tcctgtgtt cgcctgctgc tggcgccccg gggggggccaa cctctcccag gacgacagcc 240  
 agccctggac atctgtatgaa acagtgggtgg ctgggtggcac cgtgtgtctc aagtgc当地 300  
 tgaaagatca cgaggactca tccctgtcaat ggtctaaccg tgctcagcag actctctact 360  
 ttggggagaa gagagccctt cgagataatc gaattcagct ggtaacctt acgccccacg 420  
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtac acctgctcaa 480  
 tcttcactat gcctgtgcga actgc当地 agt ccctcgctcac tgtgtcttagga attccacaga 540  
 agcccatcat cactggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600  
 gtcagtc当地 tgggagcaag cctgc当地 ggtcacctg gagaaagggt gaccaagaac 660  
 tccacggaga accaaccgc当地 atacaggaag atcccaatgg taaaacccctt actgtcagca 720  
 gctcggtgac attccaggtt acccggggagg atgatggggc gagcatcgat tgctctgtga 780  
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 tacactgtga gggtc当地 gggc aatccagtc当地 cccagcagta cctatgggag aaggagggca 960  
 gtgtgccacc cctgaagatg acccaggaga gtgc当地tctgat cttcccttcc ctcaacaaga 1020  
 gtgacagtttgg cacctacggc tgacacagcca ccagcaacat gggcagctac aaggcctact 1080  
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 gtggggactg ctggggccgtt caccaacccg gacttgc当地a gagcaacccg aggccccc 1440  
 ctcccgctt cttcccccagcc cacccacccccc cctgtacaga atgctctgtt tgggtgc当地t 1500  
 tttgtactcg gtttggatg gggaggggagg agggcggggg gagggggagg ttgc当地ctc当地 1560  
 cccttccgt ggcttctctg catttgggtt attattattt ttgttaacaat cccaaatcaa 1620  
 atctgtctcc aggctggaga ggcaggagcc ctgggggtgag aaaagcaaaa aacaaacaaa 1680  
 aaaca 1685

<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Phe Ala  
 1 5 10 15

Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
 20 25 30

Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
 85 90 95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
 130 135 140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175

Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gcttaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaaat gtcaccggagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 87	
cctagcacag tgacgaggga cttggc	26
<210> 88	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 88	
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc	50
<210> 89	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 89	
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt	50
<210> 90	
<211> 2755	
<212> DNA	
<213> Homo sapiens	
<400> 90	
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ggtttccggac attggagcac taaatgaact tgaattgtgt ctgtggcgag caggatggtc 120	
gctgttactt tgtatgaga tcggggatga attgctcgct ttaaaaatgc tgctttgat 180	
tctgttgctg gagacgtctc tttgtttgc cgctggaaac gttacagggg acgtttgcaa 240	
agagaagatc tggccctgca atgagataga aggggaccta cacgttagact gtgaaaaaaaaa 300	
gggcttcaca agtctgcagc gtttactgc cccgacttcc cagtttacc atttatttct 360	
gcatggcaat tccctcactc gactttccc taatgagttc gctaactttt ataatgcgg 420	
tagtttgcac atggaaaaca atggcttgca tgaaatcggtt ccgggggctt ttctgggct 480	
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aaacggaggt acaaagatcc caggcaactg gcagatcaaa atcagaccca cagcagcgat 1140  
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 cagctgcac cacatcccag ggtcgggaaa aagatgaac tgcaacaaca ggaacgtgag 1260  
 cagcttggct gatttgaagg ccaagtcctc taacgtgcag gagctttcc tacgagataa 1320  
 caagatccac agcatccgaa aatgcactt tgtggattac aagaacctca ttctgttgg 1380  
 tctggcaac aataaacatcg ctactgtaga gaacaacact ttcaagaacc ttttgac 1440  
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 gctgcaaaac ctagagtacc tgaacgtgga gtacaacgct atccagctca tcctcccg 1560  
 cacttcaat gcatgcccc aactgaggat cctcattctc aacaacaacc tgctgagg 1620  
 cctgcctgtg gacgtgttcg ctggggctc gctctctaa ctcagcctgc acaacaatta 1680  
 cttcatgtac ctcccggtgg caggggtgct ggaccagtta acctccatca tccagataga 1740  
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 acgcttgggt tccgaagtgc tgatgagcga cctcaagtgt gagacgccc 1860  
 tagaaaggat ttcatgtcc tctccatga cgagatctc cctcagctgt acgcttaggat 1920  
 ctcgcccacg ttaacttcgc acagtaaaaa cagcactggg ttggcggaga cgggacgca 1980  
 ctccaaactcc tacctagaca ccagcagggt gtccatctc gtgttgtcc cgggactgct 2040  
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 ccgaaagcgg tccaagagac gagatccaa ctcctcccg tccgagatta attccctaca 2160  
 gacagtcgt gactcttc actggcacaa tgggccttac aacgcagatg gggcccacag 2220  
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 gcagagggaa ggcgatacat cttcccccac cgccaggacc cggggcgtg gaggggctg 2340  
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 gggcagttgc acgaaggcat gaatgtattt taaataagta actttgactt ctgac 2755

&lt;210&gt; 91

&lt;211&gt; 696

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 91

Met	Leu	Leu	Trp	Ile	Leu	Leu	Leu	Glu	Thr	Ser	Leu	Cys	Phe	Ala	Ala
1															

5

10

15

Gly	Asn	Val	Thr	Gly	Asp	Val	Cys	Lys	Glu	Lys	Ile	Cys	Ser	Cys	Asn

20

25

30

Glu	Ile	Glu	Gly	Asp	Leu	His	Val	Asp	Cys	Glu	Lys	Lys	Gly	Phe	Thr

35

40

45

Ser	Leu	Gln	Arg	Phe	Thr	Ala	Pro	Thr	Ser	Gln	Phe	Tyr	His	Leu	Phe

50

55

60

Leu	His	Gly	Asn	Ser	Leu	Thr	Arg	Leu	Phe	Pro	Asn	Glu	Phe	Ala	Asn

65

70

75

80

Phe	Tyr	Asn	Ala	Val	Ser	Leu	His	Met	Glu	Asn	Asn	Gly	Leu	His	Glu

85

90

95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
 290 295 300  
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn  
 385 390 395 400  
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn  
 405 410 415  
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser  
 420 425 430  
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn  
 435 440 445  
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro  
 450 455 460  
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
 515 520 525  
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala  
 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His  
 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

660	665	670
Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp		
675	680	685
Cys Gly Ser His Ser Leu Ser Asp		
690	695	
<210> 92		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 92		
gttggatctg ggcaacaata ac		22
<210> 93		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 93		
attgttgtgc aggctgagtt taag		24
<210> 94		
<211> 45		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 94		
ggtggtata catggatagc aattacacctgg acacgctgtc ccgggg		45
<210> 95		
<211> 2226		
<212> DNA		
<213> Homo sapiens		
<400> 95		
agtgcactgc gtccccctgtta cccggcgcca gctgtgttcc tgaccggaga ataactcagg	60	
gctgcaccgg gcctggcagc gctccgcaca catttcctgt cgccggctaa gggaaaactgt	120	
tggccgcgtgg gcccgcgggg ggattttgg cagttgggggg gtccgtcggg agcgaggggcg	180	

gaggggaagg gaggggaaac cgggttgggg aagccagctg tagagggcgg tgaccgcgt 240  
 ccagacacag ctctgcgtcc tcgagcgga cagatccaag ttggagcag ctctgcgtgc 300  
 ggggccttag agaatgaggc cggcggtcgc cctgtgcctc ctctggcagg cgctctggcc 360  
 cgggcgggc ggcggcgaac accccactgc cgaccgtgt ggctgctcg cctcggggc 420  
 ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gccgaggagg cctgcattct 480  
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 gtcctccgac cccggcggtc tcgaaagcga aacgctcgag tgggtggagg agccccaaacg 720  
 ctctgcacc ggcggagat ggcgggtact ccaggccacc ggtgggtcg agcccgagg 780  
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 ccggggacag ctcccgatct cagttacttg catgcggac gaaatcgccg ctcgcgtgg 1020  
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 aatttacatt aaaaaataat ttctacaaa atggaaagga aatgttctat gttgttcagg 2160  
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 gttgtat 2226

<210> 96  
 <211> 490  
 <212> PRT  
 <213> Homo sapiens

<400> 96  
 Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro  
 1 5 10 15

Gly Pro Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80

Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110

Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140

Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160

Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175

Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190

Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205

Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220

Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240

Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255

Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270

Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
 275 280 285

Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
 290 295 300

Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320

Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln  
 325 330 335

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

340

345

350

Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala  
 355 360 365

Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr  
 370 375 380

Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe  
 385 390 395 400

Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr  
 405 410 415

Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln  
 420 425 430

Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu  
 435 440 445

Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val  
 450 455 460

Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu  
 465 470 475 480

Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala  
 485 490

&lt;210&gt; 97

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 97

tggaaggaga tgcgatgccca cctg

24

&lt;210&gt; 98

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 98

tgaccagtgg ggaaggacag

20

<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 99  
 acagagcaga gggtgccctg 20

<210> 100  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 100  
 tcaggacaa gtggtgtctc tccc 24

<210> 101  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 101  
 tcagggagg agtgtgcagt tctg 24

<210> 102  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 102  
 acagctcccc atctcagtta cttgcattgc ggacgaaatc ggcgtcgct 50

<210> 103  
 <211> 2026  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 103

cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60  
 agcgtcgagt cagacggcac cataatcgcc tttaaaatgt cctccgcctt gcccggcg 120  
 tatccccgg ctacctgggc cgccccggc cggtgcgcgc gtgagaggga gcgcgcggc 180  
 agccgagcgc cggtgtgagc cagcgctgtc gccagtgtga gcggcggtgt gagcgcggtg 240  
 ggtgcggagg ggcgtgtgt ccggcgcgcg cggcggtgg tgcaaaaaacc 300  
 gctgcgtat ggggcgcgaa cgcctggcg ccactctgcc tgctgtggc tgccgcacc 360  
 cagctctcgc ggcagcagtc cccagagaga cctgtttca catgtggtgg cattcttact 420  
 ggagagtctg gatttattgg cagtgaaggt ttctctggag tgtaccctcc aaatagcaaa 480  
 tgtacttggaa aatcacagt tcccgaaagga aaagtagtgc ttctcaattt ccgattcata 540  
 gacctcgaga gtgacaacct gtgcgcstat gactttgtgg atgtgtacaa tggccatgcc 600  
 aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgggtccagt 660  
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 gtcacttgtg tggatggcat tggatggccaa aagaatcagc ttatagaatt aaagttttag 900  
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 gtgttatttgc ttccaccttc aagccttgc cctgaggtgt tacaatcttgc tcttgcgttt 1980  
 tctaaatcaa tgcttaataa aatattttta aaggaaaaaaa aaaaaaa 2026

&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

Met	Arg	Gly	Ala	Asn	Ala	Trp	Ala	Pro	Leu	Cys	Leu	Leu	Leu	Ala	Ala
1									10					15	

Ala	Thr	Gln	Leu	Ser	Arg	Gln	Gln	Ser	Pro	Glu	Arg	Pro	Val	Phe	Thr
													20	25	30

Cys	Gly	Gly	Ile	Leu	Thr	Gly	Glu	Ser	Gly	Phe	Ile	Gly	Ser	Glu	Gly
													35	40	45

Phe	Pro	Gly	Val	Tyr	Pro	Pro	Asn	Ser	Lys	Cys	Thr	Trp	Lys	Ile	Thr
													50	55	60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270

Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
 275 280 285

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

340	345	350
Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro		
355	360	365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu		
370	375	380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys		
385	390	395
		400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys		
405	410	415

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

<213> Homo sapiens

<400> 108  
cgacgcgtg ggccggacgcg tggcggcccc acggcgcccc cgggctgggg cggtcgcttc 60  
ttccttctcc gtggcctacg agggtccccca gctctggtaa agatggcccc atggccccc 120  
aagggcctag tccagctgt gctctggggc ctcagccctct tcctcaacct cccaggac 180  
atctggctcc agccctctcc acctccccag tttctcccc cgcctcagcc ccatccgtgt 240  
catacctgcc ggggactggt tgacagctt aacaaggccc tggagagaac catccggac 300  
aactttggag gtggaaacac tgccctggag gaagagaatt tgtccaaata caaagacagt 360  
gagaccgcgc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgcac 420  
cgccctgtgg agctgagtga ggagctggc gagagctggt gtttcacaa gcagcaggag 480  
gccccggacc tcttccagtg gctgtgtca gattccctga agctctgtc ccccgccagc 540  
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tgttcaccac atccccacac cccattgcca cttattttt catctcaggaa aataaaagaaa 1800  
qqtcttggaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly  
 1 5 10 15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser  
20 25 30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr  
 35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile  
50 55 60

Arg Asp Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
 65 70 75 80  
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
 85 90 95  
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
 100 105 110  
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125  
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
 130 135 140  
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
 145 150 155 160  
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly  
 165 170 175  
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190  
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
 195 200 205  
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220  
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240  
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
 245 250 255  
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270  
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285  
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
 290 295 300  
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320  
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335  
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
 355 360 365

Met Phe Phe Gly Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
 405 410 415

Ile Lys Gly Arg  
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 112

atctgcttgt agccctcgcc ac

22

<210> 113

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
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 cggggccgccc ctgaccgggg agcagctcct gggcagcgtg ctgcggcagc tgcatctcaa 180  
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcatccccca cccacgtgag 240  
 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagaggtt 300  
 cagccagaga ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360  
 gctgggttgc ggcattggagc agcggctgcc gccaaacagc gagctgggtgc aggccgtgct 420  
 gcggtcttc caggagccgg tccccaaggc cgctgcac aggcacgggc ggctgtcccc 480  
 gcgcaagcggc cggggccggg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540  
 ccgcacccctcc ctcatcgact ccaggctggt gtcctccac gagagcggct ggaaggcctt 600  
 cgacgtgacc gaggccgtga acttctggca gcagctgagc cggccccggc agccgctgct 660  
 gctacagggtg tcgggtcaga gggagcatct gggcccgctg gcgtccggcg cccacaagct 720  
 ggtccgctt gcctcgcagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780  
 caccctggac cttggggact atggagctca gggcgactgt gacccctgaag caccatgac 840  
 cgagggcacc cgctgctgcc gccaggagat gtacattgac ctgcaggggta tgaagtgggc 900  
 cgagaactgg gtgctggagc cccgggctt cctggcttat gagtgtgtgg gcacctggcg 960  
 gcagcccccg gaggccctgg cttcaagtg gccgttctg gggcctcgac agtgcatacg 1020  
 ctcggagact gactcgctgc ccatgatcgt cagcatcaag gaggaggca ggaccaggcc 1080  
 ccaggtggtc agectgcca acatgagggt gcagaagtgc agctgtgcct cggatgggtgc 1140  
 gctcgccca aggaggctcc agccataggc gcctagtgtt gccatcgagg gacttgactt 1200  
 gtgtgtgttt ctgaagtgtt cgagggtaacc aggagagctg gcgatgactg aactgctgat 1260  
 ggacaaatgc tctgtgtctt cttagtgacc ctgaatttgc ttccctctgac aagttacactc 1320  
 acctaatttt tgcttctcag gaatgagaat cttggccac tggagagccc ttgctcaattt 1380  
 ttctcttattt ttattattca ctgcactata ttctaaagcac ttacatgtgg agataactgta 1440  
 acctgagggc agaaaagccca ntgtgtcatt gtttacttgtt cctgtcactg gatctgggct 1500  
 aaagtccctcc accaccactc tggacctaag acctggggtt aagtgtgggt tgcataccc 1560  
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttattt ctaaaa 1616

<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala  
 1 5 10 15

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln  
 65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190

Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 115

aggactgcca taacttgcct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgcgtaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtcctt cggccggctgt tgtgtcagtgc gcctgatcgc gatggggaca 60  
 aaggcgcaag tcgagagggaa actgttgtgc ctcttcataat tggcgatcct gttgtgtcc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcaaat tcctgagaat 180

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgaaag 240  
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300  
gaggaccggg tgacccctt gccaactggg atcacccatca agtccgtgac acggaaagac 360  
actgggacat acacttgtat ggtctgttag gaaggcggca acagctatgg ggaggtcaag 420  
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctcctctgcc 480  
accattgggaa accgggact gctgacatgc tcagaacaag atggttcccc accttctgaa 540  
tacaccttgtt tcaaagatgg gatagtgtat cctacgaatc caaaaagcac ccgtgccttc 600  
agcaactctt cctatgtcct gaatcccaca acaggagagc tggctttga tccctgtca 660  
gcctctgata ctggagaata cagctgttag gcaacggaaatg ggtatggac acccatgact 720  
tcaaatgtcg tgccatggg agctgtggag cggaaatgtgg gggtcatcg tgcagccgtc 780  
cttgtAACCC tgattcttctt gggaaatctt gtttttggca tctggttgc ctatagccga 840  
ggccactttg acagaacaaa gaaaggact tegagtaaga aggtgattt aagccagcct 900  
agtccccaa gtgaaggaga attcaaacag acctcgatcat tcctgggtgt agcctggtcg 960  
gctcaccgccc tatcatctgc atttgcctt ctcagggtgtt accggactct ggccccctgat 1020  
gtctgttagtt tcacaggatg ctttattttgtt cttctacacc ccacaggccc ccctacttct 1080  
tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cctccctccc 1140  
tttcctacca ctgctgagtg gcctggaaact tgtttaaagt gtttattccc catttcttgc 1200  
agggatcagg aaggaatctt gggtatgcca ttgacttccc ttctaagtag acagaaaaaa 1260  
tggcgggggt cgccaggatc tgcactcaac tgccccaccc gctggcaggg atcttgaat 1320  
aggtatcttg agcttggttc tgggctttt cttgtgtac tgacgaccag ggccagctgt 1380  
tctagagcgg gaatttagagg ctagagcggc tggaaatgggt gtttgggtat gacactgggg 1440  
tccttcatc tctggggccc actcttttctt gtcttccat gggaaatgccc actgggatcc 1500  
ctctgcctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaaatggg 1560  
agctctgtt gtggagagca tagtaaattt tcaagagaact tgaagccaaa aggatttaaa 1620  
accgctgtcc taaagaaaaag aaaactggag gctggcgcga gtggctcagc cctgtatcc 1680  
cagaggctga ggcaggcggc tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740  
ggagaaaaacc tactggaaat acaaagttt ccaggcatgg tggtgcatgc ctgttagtccc 1800  
agctqctcaq qaqcctggca acaagagcaa aactccagct caaaaaaaaaaa aaaaaaaaaa 1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
 245 250 255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
 260 265 270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
 275 280 285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
 290 295

&lt;210&gt; 120

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 120

tcgcggagct gtgttctgtt tccc

&lt;210&gt; 121

&lt;211&gt; 50

<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 121		
tgatcgcat ggggacaaag gcgcaggctc gagaggaaac ttttgcct		50
<210> 122		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 122		
acacacctggtt caaagatggg		20
<210> 123		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 123		
taggaagagt tgctgaaggc acgg		24
<210> 124		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 124		
ttgccttact caggtgctac		20
<210> 125		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		

## oligonucleotide probe

<400> 125  
actcagcagt ggttagaaag 20

<210> 126  
<211> 1210  
<212> DNA  
<213> Homo sapiens

<400> 126  
cagcgcgtgg ccggcgccgc tggggaca gcatgagcgg cggtggatg ggcagggtt 60  
gagcgtggcg aacaggggct ctgggcctgg cgctgctgt gctgctggc ctcggactag 120  
gcctggaggc cgccgcgagc cccgtttcca cccgcaccc tgcccaaggcc gcaggcccc 180  
gctcaggctc gtgcccaccc accaagtcc agtgcgcac cagtggtta tgcgtgcccc 240  
tcacctggcg ctgcgacagg gacttggact gcaagcgatgg cagcgatgag gaggagtgca 300  
ggattgagcc atgtacccag aaaggcaat gcccaccgc ccctggcctc ccctgccct 360  
gcacccggcgt cagtgactgc tctggggaa ctgacaagaa actgcgcac acgcggcc 420  
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480  
ggcgtgcga cggccaccca gactgtcccg actccagcga cgagctggc tggaaacca 540  
atgagatcct cccggaagg gatgccacaa ccatggggcc ccctgtgacc ctggagagt 600  
tcacctctct caggaatgcc acaaccatgg ggcccccgt gaccctggag agtgtccct 660  
ctgtcggaa tgccacatcc tcctctggc gagaccagtc tggaaagccca actgcctatg 720  
gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgcacc ctcccttt 780  
tgtcctggct cggagcccg gagcgcctcc gcccactgg gttactggg gccatgaagg 840  
agtccctgtct gctgtcagaa cagaagacct cgctgcccgt aggacaagca cttgccacca 900  
ccgtcaactca gcccctggcg tagccggaca ggaggagagc agtgtatgcgg atgggtaccc 960  
gggcacaccca gcccctcagag acctgagttc ttctggccac gtggAACCTC gaacccgagc 1020  
tcctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080  
agcttaggatg gggAACCTGC cacagccaga actgaggggc tggcccccagg cagctccct 1140  
ggggtagaaac gcccctgtgc ttaagacact ccctgctgccc cctgctgagg gtggcgatta 1200  
aagttgcttc 1210

<210> 127  
<211> 282  
<212> PRT  
<213> Homo sapiens

<400> 127  
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln  
                   85                  90                  95

Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly  
                   100              105                  110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser  
                   115              120                  125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp  
                   130              135                  140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp  
                   145              150                  155                  160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly  
                   165              170                  175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser  
                   180              185                  190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val  
                   195              200                  205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly  
                   210              215                  220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala  
                   225              230                  235                  240

Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln  
                   245              250                  255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu  
                   260              265                  270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro  
                   275              280

<210> 128  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 128  
 aagttccagt gccgcaccag tggc

<210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 129  
 ttggttccac agccgagctc gtcg 24

<210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaaggc aatgccacc 50

<210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1837)  
 <223> a, t, c or g

<400> 131  
 cccacgcgtc cggtctcgct cgctcgcgca gccccggcag cagaggtcgc gcacagatgc 60  
 gggtagact ggcgggggggaa ggaggcggag gagggaaagga agctgcgtgc atgagaccca 120  
 cagactcttg caagctggat gcccctgtgt gatgaaaagat gtatcatgga atgaacccga 180  
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240  
 gactcttggc cgtgatcctg tggttgcagc tggcgctgtg ctccggccct gcacagctca 300  
 cggccgggtt cgatgacctt caagtgtgtg ctgacccgg cattcccgag aatggcttca 360  
 ggaccccccag cggagggggtt ttctttgaag gctctgttagc ccgatttcac tgccaagacg 420  
 gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcatttaat ggaaccctag 480  
 gctggatccc aagtgataat tccatctgtg tgcaagaaga ttggcgatc cctcaaatcg 540  
 aagatgctga gattcataac aagacatata gacatggaga gaagctaattt atcaacttgtc 600  
 atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcatca tgtcgcgtat 660  
 atggAACGTG gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720  
 atggctatgt aaacatctt gagctccaga cctccttccc ggtggggact gtgatctcct 780  
 atcgctgctt tcccgattt aaacttgtat ggtctgcgtt tcttgagtgc ttacaaaacc 840  
 ttatctggtc gtccagccca cccccgggtcc ttgtctgttggaa agcccaagtc tgcactac 900  
 ctccaatggt gagtcacgga gatttcgtct gcccacccggc gccttgcgttgc cgctacaacc 960  
 acggaactgt ggtggagtt tactgcgtac ctggctacag cctcaccaggc gactacaagt 1020  
 acatcacctg ccagttatggaa gatgttttcc ttctttatca agtctactgc atcaaatcag 1080  
 agcaaacgtg gcccagcacc catgagaccc tcctgaccac gtggaaagatt gtggcggttca 1140

cgccaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200  
 agttcaaggc ccacttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260  
 ttgtggtgtt agacggcggt cccgtcatgc tccctgttcata tgacgaagct gtgagtggcg 1320  
 gcttgagtgc cttaggcccc gggtacatgg cctctgtggg ccagggctgc cccttacccg 1380  
 tggacgacca gagcccccca gcataccccc gctcaggggg cacggacaca gggccagggg 1440  
 agtcagaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500  
 ctcccagggtg ccaagagagc acccaccctg cttcggacaa ccctgacata attgccagca 1560  
 cggcagagga ggtggcatcc accagcccag gcatccatca tgcccactgg gtgttgtcc 1620  
 taagaaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680  
 gttgatctgt ggagttgatt ccttccttc tcttggttt agacaaatgt aaacaaagct 1740  
 ctgatcctta aaattgctat gctgatagag tggtgagggc tggaagctg atcaagtcc 1800  
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

&lt;210&gt; 132

&lt;211&gt; 490

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 132

Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln
1															15

5

10

15

Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val
20														30

20

25

30

Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr
35															45

35

40

45

Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu
50															60

50

55

60

Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val
65															80

65

70

75

80

Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys
85															95

85

90

95

Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser
100															110

100

105

110

Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu
115															125

115

120

125

Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile
130															140

130

135

140

Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn
145															160

145

150

155

160

Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile
165															175

165

170

175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr		
195	200	205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys		
210	215	220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu		
225	230	235
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe		
245	250	255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val		
260	265	270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr		
275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
450	455	460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133

atctcctatac gctgctttcc cggt

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135

atttaaacctt gatgggtctg cgtatcttga gtgcttacaa aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gcctcccggtg cggccgtcg gtggcctaga 60

gatgtgtctg cgcgggttcg agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120

ccgttagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180

tacaggccgt gctgtggcc gtgctgtgg tggttgtcgg ggcgcgacg ggtcgcctgc 240

tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgcggggga gggacacaga 300

ggccttgta taaagtcatt tactccatg atacttctcg aagactgaac tttgaggaag 360  
ccaaaagaagc ctgcaggagg gatggaggcc agctagtca gatcgactt gaagatgaac 420  
agaaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgtgac ttctggattg 480  
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgcccaggac ctttatgctt 540  
ggactgatgg cagcatatca caattttaga actggtatgt ggatgagccg tcctgcggca 600  
gchgaggtctg cgtggcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660  
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaataatt 720  
ctgatgagaa accagcagtt ccttcttagag aagctgaagg tgagggaaaca gagctgacaa 780  
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaaagta 840  
gagaagctgc cttaaatctg gcctacatcc taatccccag cattccctt ctccctccccc 900  
tttgtgtcac cacagttgt a tttgggtt ggatctgtag aaaaagaaaa cgggagcagc 960  
cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag gaaaacagcc 1020  
cgAACCTAGA ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080  
ggccagacct gaagaatatt tcattccgag tttgttcggg agaagccact cccgatgaca 1140  
tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggtt gtgactctgg 1200  
tgagcgtgga gagtggattt gtgaccaatg acatttatga tttctccca gaccaaatgg 1260  
ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaaa 1320  
aaactgaaac tgacaacaat ggaaaagaaaa tgataagcaa aatcccttta tttctataa 1380  
ggaaaataca cagaaggct atgaacaagc tttagatcagg tcctgtggat gagcatgtgg 1440  
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tccagctcga ccttatgaga aggtacccctg cccaggtctg gcacatagta gagtctcaat 1560  
aaatgtcact tgggtgggtt tatctaactt ttaagggaca gagctttacc tggcagtgt 1620  
aaagatggc tgggagctt ggaaaaccac ctctgtttt cttgtcttat acagcagcac 1680  
atattatcat acagacagaa aatccagaat ctttcaaaag cccacatatg gtgcacagg 1740  
ttggcctgtg catcgccaaat tctcatatct gttttttca aagaataaaa tcaaataaaag 1800  
aqaqqaaaa aaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val 10 Leu Leu Ala Val 15 Leu

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
 65                    70                    75                    80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125

Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140

Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160

Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175

Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190

Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205

Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220

Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240

Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255

Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270

Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285

Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300

Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320

Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335

Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350

Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365

Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 140  
 cagtccaagc ataaaggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgccg acttgggggc gcccgcgtgag ccccgccgcg ccgcagaagac 120  
 ttgtgtttgc ctccctgcagc ctcaaccggc agggcagcga gggcctacca ccatgatcac 180  
 tggtgtgttc agcatgcgtc tgtggacccc agtggggcgtc ctgacctcgc tggcgtaactg 240  
 cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcggt tttcgacacg gggctcgag 360  
 tcctctcaag ccgcctccgc tggaggagca ggttagatgg aacccccagc tattagaggt 420  
 cccaccccaa actcagttt attacacagt caccaatcta gctgggtggc cgaaaccata 480  
 ttctcccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctggca 540  
 gctgaccaag gtgggcattgc agcaaatgtt tgccttgga gagagactga ggaagaacta 600  
 tgtggaagac attcccttgc tttcaccaac cttcaaccca caggaggctt ttattcggtc 660  
 cactaacatt tttcgaaatc tggagtccac ccgttgtttg ctggctggc tttccagtg 720

tcagaaaagaa ggacccatca tcatccacac tcatgaagca gattcagaag tcttgatcc 780  
 caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840  
 tttacagcca ggaatctcag aggattgaa aaaggtgaag gacaggatgg gcattgacag 900  
 tagtgataaa gtggacttct tcatacctcct ggacaacgtg gctgccgagc aggcacacaa 960  
 cctcccaagc tgccccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020  
 cacatccttg tacatactgc ccaaggaaga cagggaaagt cttagatgg cagtagggcc 1080  
 attccctccac atccttagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140  
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200  
 gaccctgggg attttgacc acaaattggcc accgtttgtt gttgacactga ccatggact 1260  
 ttaccagcac ctggaatcta aggagtggtt tgtgcagctc tattaccacg ggaaggagca 1320  
 ggtgccgaga gtttgcctg atggctctg cccgctggac atgttcttga atgccatgtc 1380  
 agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaactc aggtgatgga 1440  
 agttgaaat gaagagtaac tgatttataa aagcaggatg tggatgttt aaaataaagt 1500  
 gccttatac aatg 1514

&lt;210&gt; 142

&lt;211&gt; 428

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

Met	Ile	Thr	Gly	Val	Phe	Ser	Met	Arg	Leu	Trp	Thr	Pro	Val	Gly	Val
1				5					10				15		

Leu	Thr	Ser	Leu	Ala	Tyr	Cys	Leu	His	Gln	Arg	Arg	Val	Ala	Leu	Ala
								20				25			30

Glu	Leu	Gln	Glu	Ala	Asp	Gly	Gln	Cys	Pro	Val	Asp	Arg	Ser	Leu	Leu
								35			40			45	

Lys	Leu	Lys	Met	Val	Gln	Val	Val	Phe	Arg	His	Gly	Ala	Arg	Ser	Pro
								50			55			60	

Leu	Lys	Pro	Leu	Pro	Leu	Glu	Glu	Gln	Val	Glu	Trp	Asn	Pro	Gln	Leu	
								65			70			75		80

Leu	Glu	Val	Pro	Pro	Gln	Thr	Gln	Phe	Asp	Tyr	Thr	Val	Thr	Asn	Leu
								85			90			95	

Ala	Gly	Gly	Pro	Lys	Pro	Tyr	Ser	Pro	Tyr	Asp	Ser	Gln	Tyr	His	Glu
								100			105			110	

Thr	Thr	Leu	Lys	Gly	Gly	Met	Phe	Ala	Gly	Gln	Leu	Thr	Lys	Val	Gly
								115			120			125	

Met	Gln	Gln	Met	Phe	Ala	Leu	Gly	Glu	Arg	Leu	Arg	Lys	Asn	Tyr	Val
								130			135			140	

Glu	Asp	Ile	Pro	Phe	Leu	Ser	Pro	Thr	Phe	Asn	Pro	Gln	Glu	Val	Phe	
								145			150			155		160

Ile	Arg	Ser	Thr	Asn	Ile	Phe	Arg	Asn	Leu	Glu	Ser	Thr	Arg	Cys	Leu
								165			170			175	

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425  
 <210> 143  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143  
ccaactacca aagctgctgg agcc 24

<210> 144  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144  
gcagctctat taccacggga agga 24

<210> 145  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145  
tccttccgt gtaatagag ctgc 24

<210> 146  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146  
ggcagagaac cagaggccgg aggagactgc ctcttacag ccagg 45

<210> 147  
<211> 1686  
<212> DNA  
<213> Homo sapiens

<400> 147  
ctcctcttaa catacttgca gctaaaacta aatattgtg cttggggacc tccttcttagc 60  
cttaaatttc agtcatacac cttcacctgc cttgggtcatg gctctgtat tctcattgtat 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtggg 180

gggcctccac cgctgtgaag ggcgggtgga ggtggAACAG aaaggCCAGT ggggcaccgt 240  
gtgtatgac ggctggaca ttaaggacgt ggctgtgtt tgccggagc tggctgtgg 300  
agctgccAGC ggaACCCCTA gtggTATTT gtatgagcc caAGCAGAAA aAGAGCAAAA 360  
ggtcctcatc caatcagtca gttgcacagg aacagaAGAT acattggCTC agtgtgAGCA 420  
agaagaAGTT tatgattgtt cacatgatga agatgCTGGG gcatcgTGT agaACCCAGA 480  
gagctCTTC tccccAGTCC cagaggGTGT caggCTGGT gacggCCCTG ggcattgCAA 540  
gggacgcgtg gaagtgaAGC accagaACCA gtggtaTACc gtgtGCCAGA caggCTGGAG 600  
cctccgggCC gcaaaggTGG tgtGCCGGCA gctgggatgt gggaggGCTG tactgactCA 660  
aaaacgCTGC aacaaggCATG cctatggCCG aaaACCCATC tggctgAGCC agatgtCATG 720  
ctcaggacga gaagcaACCC ttCaggATTG cccttCTGGG cttggggGA agaACACCTG 780  
caaccatgat gaagacacGT gggTCGAATG tgaAGATCCC ttgacttGA gacttagGAG 840  
aggagacaAC ctctgCTCG ggcgactGGA ggtgCTGCAC aaggGCGTAT ggggCTCTGT 900  
ctgtatgac aactggggAG aaaaggAGGA ccaggTGGTA tgcaAGCAAC tggctgtgg 960  
gaagtCCCTC tctccCTCT tcagagACCG gaaatgCTAT ggcctgggg ttggccgcat 1020  
ctggCTGGAT aatgttCGTt gctcaggGGGA ggagcAGTCC ctggagcAGT gccagcacAG 1080  
atTTTggggg tttcacgact gcacCCACCA ggaAGATGT gctgtcatCT gtcAGTGTa 1140  
ggtgggcATC atctaATCTG ttgagtgcCT gaatAGAAGA aaaACACAGA agaAGGGAGC 1200  
atTTACTGTC tacatgACTG catggatGA acactgatCT tcttCTGCCC ttggactGGG 1260  
acttataACTT ggtggcccCTG attctcAGGC cttcagAGT ggatcAGAAAC ttacaACATC 1320  
aggTCTAGTT ctcaggCCAT cagacatAGT ttggAAACTAC atcaccACCT ttccTATGTC 1380  
tccacattGC acacAGCAGA ttcccAGCCT ccataATTGT gtgtatCAAC tactAAATA 1440  
cattCTCACA cacacACACA cacACACACA cacACACATAA ccatTTGTCC 1500  
tgTTTCTCTG aagaACTCTG acaaAAataCA gatTTGGTA ctgaaAGAGA ttctAGAGGA 1560  
acggaATTTT aaggataAAAT ttTCTGAATT ggttatGGGG ttTCTGAAT tggctCTATA 1620  
atctaATTAG atataAAATT ctggtaACTT tatttacaAT aataAAAGATA gcactatGTG 1680  
ttcaAA 1686

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met	Ala	Leu	Leu	Phe	Ser	Leu	Ile	Leu	Ala	Ile	Cys	Thr	Arg	Pro	Gly
1					5					10					15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
                   20                  25                  30

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
           50                 55                 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
          95             90                         95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Glu Gln Glu Val Tyr  
100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 149 ttcagtcat cacccacc tgcc	24
<210> 150 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 150 ggctcataca aaataccact aggg	24
<210> 151 <211> 50 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 151 gggcctccac cgctgtgaag ggccgggtgga ggtggAACAG aaaggccagt	50
<210> 152 <211> 1427 <212> DNA <213> Homo sapiens	
<400> 152 actgcactcg gttcttatcga ttgaattccc cggggatcct ctagagatcc ctgcaccccg 60 acccacgcgt ccgcggacgc gtggccggac gcgtggcccg gctaccagga agagtctgcc 120 gaagggtgaag gccatggact tcacccatc cacagccatc ctgcacctgc tgccggctg 180 cctggcgctc ttcggccctt tccggctgct gcagtgggtg cgccggaaagg cctacctgcg 240 aatgtgtg gtgggtatca caggcgccac ctcaggctg ggcaaagaat gtgaaaagt 300 cttcttatgct gccccgtcta aactggtgct ctgtggccgg aatgggtgggg ccctagaaga 360 gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420 ggtgacccctc gacccatcg actctgggc catagttgca gcagcagctg agatcctgca 480 gtgtttggc tatgtcgaca tacttgtcaa caatgtggg atcagctacc gtggtaccat 540 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccggt 600 tgctctaacg aaagcactcc tgccctccat gatcaagagg agccaaggcc acattgtcgc 660 catcagcagc atccaggcgca agatgagcat tcctttcga tcagcatatg cagcctccaa 720 gcacgcaacc caggctttct ttgactgtct gcgtggccgg atgaaacagt atgaaattga 780 ggtgaccgtc atcagccccg gctacatcca caccaaccc tctgtaaatg ccatcaccgc 840 ggatggatct aggtatggag ttatggacac caccacagcc caggccggaa gcccgtggaa 900 ggtgcccgatgttcttgcgtgtggg gaagaagaag aaagatgtga tcctggctga 960 cttactgcct tccttggctg tttatctcg aactctggct cctggctct tcttcagcct 1020 catggcctcc agggccagaa aagagcggaa atccaagaac tccttagtact ctgaccagcc 1080	

agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcac 1140  
 ttgtttagac ttaatggag atttgtctca caagtggaa agactgaaga aacacatctc 1200  
 gtgcagatct gctggcagag gacaatcaa aacgacaaca agcttcttcc cagggtgagg 1260  
 ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaaca 1320  
 tctcaaacag taaaaaaaaaaa aaaaaaggc gcgcgact cttagatcga cctgcagaag 1380  
 cttggccgccc atggcccaac ttgtttattt cagcttataa tggttac 1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys  
 1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys  
 20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Ile Thr Gly Ala Thr Ser Gly  
 35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu  
 50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu  
 65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu  
 85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala  
 100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala  
 115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp  
 130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys  
 145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala  
 165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr  
 180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala  
 195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235
Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
245	250	255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Asp Val		
260	265	270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
275	280	285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
290	295	300
Arg Lys Ser Lys Asn Ser		
305	310	

&lt;210&gt; 154

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 154

ggtgctaaac tggtgctctg tggc

24

&lt;210&gt; 155

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 155

caggccaaga tgagcattcc

20

&lt;210&gt; 156

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 156		
tcatactgtt ccatctcgcc acgc		24
<210> 157		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 157		
aatgggggg ccctagaaga gctcatcaga gaactcacccg cttctcatgc		50
<210> 158		
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<212> DNA		
<213> Homo sapiens		
<400> 158		
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<210> 159		

&lt;211&gt; 300

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

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1			5				10							15	

Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys
			20				25					30			

Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
					35			40				45			

Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
	50					55			60						

Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
	65				70			75						80	

Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
					85			90				95			

Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
			100				105					110			

Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
	115					120			125						

Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
	130				135				140						

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
	145				150			155					160		

Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
					165			170					175		

Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
				180				185				190			

Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile
	195				200								205		

Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
	210				215				220						

Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
	225				230			235			240				

Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
				245				250				255			

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 161

atcccatgca tcagcctgtt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 162

gctgggttag tctatacacatc agatttgttt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

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 tcagggagga gcaccgactg cggccaccc tgagagatgg ttggtgccat gtgaaagggtg 120

attgttcgc tggcctgtt gatgcctggc ccctgtatg ggctgtttcg ctccctatac 180  
 agaagtgtt ccatgccacc taaggagac tcaggacagc cattattct cacccttac 240  
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttccagga 300  
 ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360  
 ttcttcttgtt tcttccagc tcagatacag ccagaagatg ccccaagtagt tctctggcta 420  
 cagggtggc cgggaggtc atccatgtt ggactcttg tggAACATGG gccttatgtt 480  
 gtcacaagta acatgacattt gcgtacaga gacttccctt ggaccacaac gctctccatg 540  
 ctttacattt acaatccagt gggcacaggc ttcagtttta ctgtgatac ccacggat 600  
 gcagtcaatg aggacgatgt agcacggat ttatacagtg cactaattca gttttccag 660  
 atatttcctg aatataaaaa taatgacttt tatgtactg gggagtctta tgcagggaaa 720  
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780  
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 tttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaa 1200  
 ccatggtaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260  
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 ataatagttt tggggaaaaag attctcaaattt gtataaagtc ttggaaacaaa agaattctt 2040  
 gaaataaaaaa tattatatat aaaagtaaaa aaaaaaa 2076

&lt;210&gt; 164

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 164

Met	Val	Gly	Ala	Met	Trp	Lys	Val	Ile	Val	Ser	Leu	Val	Leu	Leu	Met
1									10					15	

Pro	Gly	Pro	Cys	Asp	Gly	Leu	Phe	Arg	Ser	Leu	Tyr	Arg	Ser	Val	Ser
									20				25		30

Met	Pro	Pro	Lys	Gly	Asp	Ser	Gly	Gln	Pro	Leu	Phe	Leu	Thr	Pro	Tyr
									35				40		45

Ile	Glu	Ala	Gly	Lys	Ile	Gln	Lys	Gly	Arg	Glu	Leu	Ser	Leu	Val	Gly
									50				55		60

Pro	Phe	Pro	Gly	Leu	Asn	Met	Lys	Ser	Tyr	Ala	Gly	Phe	Leu	Thr	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65	70	75	80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Pro Ala Gln			
85		90	95
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro			
100		105	110
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val			
115		120	125
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr			
130		135	140
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser			
145		150	155
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala			
165		170	175
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu			
180		185	190
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195		200	205
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210		215	220
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225		230	235
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245		250	255
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His			
260		265	270
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275		280	285
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290		295	300
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305		310	315
320			
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325		330	335
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340		345	350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
465 470 475

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<210> 165
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 165  
ttccatgcc a cctaaggag actc

24

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<210> 166
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 166  
tggatgaggt gtgcaatggc tggc

24

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<210> 167
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 167  
 agctctcaga ggctggtcat aggg 24  
  
 <210> 168  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 168  
 gtcggccctt tcccaggact gaacatgaag agttatgcgg gcttcctcac 50  
  
 <210> 169  
 <211> 2477  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 169  
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acatctgcaa	aagcaaa					2477

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

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 20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu  
35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala  
50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val  
65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His  
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly  
100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr  
115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp  
120 125

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val  
115

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys  
 180 185 190

Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys  
 195 200 205

Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
 210 215 220

Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr  
 225 230 235 240

Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys  
 245 250 255

Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His  
 260 265 270

Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala  
 275 280 285

Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly  
 290 295 300

Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val  
 305 310 315 320

Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg  
 325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe  
 340 345 350

Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr  
 355 360 365

Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser  
 370 375 380

Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr  
 385 390 395 400

His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
 405 410 415

Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu  
 420 425 430

Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
 435 440 445

Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

100

450                    455                    460  
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
465                    470                    475                    480  
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
485                    490                    495  
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
500                    505                    510  
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
515                    520                    525  
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
530                    535                    540  
Leu Tyr Phe Leu Gly Glu Gln Arg  
545                    550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171

tggaaataccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 173  
 ggactcactg gcccaggcct tcaatatac cagccaggac gat  
  
 <210> 174  
 <211> 3106  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> modified\_base  
 <222> (1683)  
 <223> a, t, c or g  
  
 <400> 174  
 aggctccgc gcgcggctga gtgcggactg gagtggaaac ccgggtcccc gcgcttagag 60  
 aacacgcgt gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120  
 tgctggctgt ctgggcttc ctgggtctcc gcaggctgga ctggagcacc ctggccctc 180  
 tgcggctccg ccatcgacag ctggggctgc aggccaaggg ctggaaacttc atgctggagg 240  
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 ggagggacccg cctgtgaag atgaaggcct gtggcttcaa caccctcacc acctatgttc 360  
 cgtggAACCT gcatgagcca gaaagaggca aatttgactt ctctggaaac ctggacctgg 420  
 aggccttcgt cctgtggcc gcagagatcg ggctgtgggt gattctgcgt ccaggcccct 480  
 acatctgcag tgagatggac ctgggggct tgccctggctg gctactccaa gaccctggca 540  
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 ttagtccag ggtggtgcca ctccagtaca acgtggggg acctatcatt gccgtgcagg 660  
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 cactggagga cctgtggcatt gtggaaactgc tcctgacttc agacaacaag gatgggttga 780  
 gcaagggat tggccaggaa gtcttggcca ccatcaactt gcaactcaaca cacgagctgc 840  
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 atgtcaccag ctatgactat gatgtgtgc tgacagaagc cggcgattac acggccaaat 1140  
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 ggctcaactgt cctgagttgc agtaaagcta taaccttgaa tcacaa 3106

&lt;210&gt; 175

&lt;211&gt; 636

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (539)

&lt;223&gt; Any amino acid

&lt;400&gt; 175

Met	Thr	Thr	Trp	Ser	Leu	Arg	Arg	Arg	Pro	Ala	Arg	Thr	Leu	Gly	Leu
1															15

Leu	Leu	Leu	Val	Val	Leu	Gly	Phe	Leu	Val	Leu	Arg	Arg	Leu	Asp	Trp
															30
20								25							

Ser	Thr	Leu	Val	Pro	Leu	Arg	Leu	Arg	His	Arg	Gln	Leu	Gly	Leu	Gln
															45
35							40								

Ala	Lys	Gly	Trp	Asn	Phe	Met	Leu	Glu	Asp	Ser	Thr	Phe	Trp	Ile	Phe
															60
50								55							

Gly	Gly	Ser	Ile	His	Tyr	Phe	Arg	Val	Pro	Arg	Glu	Tyr	Trp	Arg	Asp
															80
65								70			75				

Arg	Leu	Leu	Lys	Met	Lys	Ala	Cys	Gly	Leu	Asn	Thr	Leu	Thr	Thr	Tyr
															95
85										90					

Val	Pro	Trp	Asn	Leu	His	Glu	Pro	Glu	Arg	Gly	Lys	Phe	Asp	Phe	Ser
															110
100								105							

Gly	Asn	Leu	Asp	Leu	Glu	Ala	Phe	Val	Leu	Met	Ala	Ala	Glu	Ile	Gly
															125
115								120							

Leu	Trp	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ser	Glu	Met	Asp
															140
130								135							

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160  
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175  
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190  
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205  
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220  
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240  
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
 245 250 255  
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 270  
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285  
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300  
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320  
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335  
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350  
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365  
 Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380  
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400  
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415  
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
 435                    440                    445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
 450                    455                    460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
 465                    470                    475                    480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
 485                    490                    495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
 500                    505                    510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
 515                    520                    525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
 530                    535                    540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
 545                    550                    555                    560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
 565                    570                    575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
 580                    585                    590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
 595                    600                    605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
 610                    615                    620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
 625                    630                    635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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 aaggggagca aagccgggct cggcccaggc cccccaggac ctccatctcc caatgttgaa 180  
 ggaatccgac acgtgacggt ctgtccqccg tctcagacta gagggagcgct gtaaacgcca 240  
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 tgctgccccca ggcagacact cggtcggtcg tagtggatag gggtcatgac cggtttctcc 360  
 tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctacttcgg gtaccgcggg 420

tgcttggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagttt 480  
atgtccctg gaactaccac gagccacagc ctggggctta taacttaat ggcagccgg 540  
acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600  
gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctggttg cttcgaaaac 660  
ctgaaattca tctaagaacc tcagatccag acttccttgc cgcatggac tcctggttca 720  
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tccagcctgg ctgacagtga gacactccat ctcaaaaaaaaaaaaa 2505

&lt;210&gt; 177

&lt;211&gt; 654

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 177

Met	Ala	Pro	Lys	Lys	Leu	Ser	Cys	Leu	Arg	Ser	Leu	Leu	Leu	Pro	Leu
1														15	

Ser	Leu	Thr	Leu	Leu	Pro	Gln	Ala	Asp	Thr	Arg	Ser	Phe	Val	Val
													30	

Asp	Arg	Gly	His	Asp	Arg	Phe	Leu	Leu	Asp	Gly	Ala	Pro	Phe	Arg	Tyr
													45		

Val	Ser	Gly	Ser	Leu	His	Tyr	Phe	Arg	Val	Pro	Arg	Val	Leu	Trp	Ala
												50	60		

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe  
 65 70 75 80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe  
 85 90 95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala  
 100 105 110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp  
 115 120 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His  
 130 135 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe  
 145 150 155 160

Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly  
 165 170 175

Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala  
 180 185 190

Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu  
 195 200 205

Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu  
 210 215 220

Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Val Asp Phe Gly Pro  
 225 230 235 240

Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro  
 245 250 255

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr  
 260 265 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly  
 275 280 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe  
 290 295 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly  
 305 310 315 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser  
 325 330 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350	
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro			
355	360	365	
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu			
370	375	380	
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu			
385	390	395	400
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr			
405	410	415	
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val			
420	425	430	
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val			
435	440	445	
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr			
450	455	460	
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg			
465	470	475	480
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro			
485	490	495	
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu			
500	505	510	
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys			
515	520	525	
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr			
530	535	540	
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly			
545	550	555	560
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr			
565	570	575	
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu			
580	585	590	
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu			
595	600	605	
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu			
610	615	620	

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala  
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His  
 645 650

<210> 178  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 178  
tggctactcc aagaccctgg catg 24

<210> 179  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 179  
tggacaaatc cccttgctca gccc 24

<210> 180  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 180  
gggcttcacc gaagcagtgg acctttatcc tgaccacctg atgtccaggg 50

<210> 181  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 181  
ccagctatga ctatgatgca cc 22

<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 182  
 tggcacccag aatggtgtt gctc 24

<210> 183  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt cctttggac cttaacctcc 50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

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 aatattcttt cgaaaaagtc agagaagaga gcagtttag tgacattcca gatgtcaaaa 240  
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 agggaaaggaa aaattataat cactaatctt ggttctttt aaattgtttg taacttgat 1860  
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 ttttcttact aaaaaaaaaaaaaaaa 1947

<210> 185  
 <211> 501  
 <212> PRT  
 <213> Homo sapiens

<400> 185															
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Cys	Val	Tyr	Gly	Phe	Ile	Cys	Leu	Tyr	Thr	Leu	Phe	Trp	Leu	Phe	Arg
					20			25					30		
Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser
					35			40				45			
Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His
					50			55				60			
Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
					65			70				75			80
Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His
					85					90			95		
Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln
					100			105				110			
Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala
					115			120				125			
Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro
					130			135				140			
Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu
					145			150				155			160
Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser
					165				170				175		
Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val
					180			185				190			

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465	470	475	480
-----	-----	-----	-----

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro			
	485	490	495

Phe Ala Asn Gly Ile  
500

&lt;210&gt; 186

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 186

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21

&lt;210&gt; 187

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 187

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24

&lt;210&gt; 188

&lt;211&gt; 47

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 188

gtcacatttat ttctcttaaca acaagctcga atccttacca gtggcag

47

&lt;210&gt; 189

&lt;211&gt; 2917

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 189

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aagacatttg tgtttacac acataaggat ctgtgtttgg ggtttcttct tcctccctg 180

gcattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgct 240  
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agaagaaaagg cacagctccc catcagttc atggaaaata actcaigtcc tgctggaaac 720  
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<210> 190

211 <211> 607

<212> PRT

<213> Homo sapiens

<400> 190

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Cys	Leu	Ala	Glu	Leu	Thr	Met	Ala	Glu	Ala	Glu	Gly	Asn	Ala	Ser	Cys
						20				25					30
Thr	Val	Ser	Leu	Gly	Gly	Ala	Asn	Met	Ala	Glu	Thr	His	Lys	Ala	Met
						35				40					45
Ile	Leu	Gln	Leu	Asn	Pro	Ser	Glu	Asn	Cys	Thr	Trp	Thr	Ile	Glu	Arg
						50				55					60
Pro	Glu	Asn	Lys	Ser	Ile	Arg	Ile	Ile	Phe	Ser	Tyr	Val	Gln	Leu	Asp
						65				70					80
Pro	Asp	Gly	Ser	Cys	Glu	Ser	Glu	Asn	Ile	Lys	Val	Phe	Asp	Gly	Thr
						85				90					95
Ser	Ser	Asn	Gly	Pro	Leu	Leu	Gly	Gln	Val	Cys	Ser	Lys	Asn	Asp	Tyr
						100				105					110
Val	Pro	Val	Phe	Glu	Ser	Ser	Ser	Ser	Thr	Leu	Thr	Phe	Gln	Ile	Val
						115				120					125
Thr	Asp	Ser	Ala	Arg	Ile	Gln	Arg	Thr	Val	Phe	Val	Phe	Tyr	Tyr	Phe
						130				135					140
Phe	Ser	Pro	Asn	Ile	Ser	Ile	Pro	Asn	Cys	Gly	Gly	Tyr	Leu	Asp	Thr
						145				150					160
Leu	Glu	Gly	Ser	Phe	Thr	Ser	Pro	Asn	Tyr	Pro	Lys	Pro	His	Pro	Glu
						165				170					175
Leu	Ala	Tyr	Cys	Val	Trp	His	Ile	Gln	Val	Glu	Lys	Asp	Tyr	Lys	Ile
						180				185					190
Lys	Leu	Asn	Phe	Lys	Glu	Ile	Phe	Leu	Glu	Ile	Asp	Lys	Gln	Cys	Lys
						195				200					205
Phe	Asp	Phe	Leu	Ala	Ile	Tyr	Asp	Gly	Pro	Ser	Thr	Asn	Ser	Gly	Leu
						210				215					220
Ile	Gly	Gln	Val	Cys	Gly	Arg	Val	Thr	Pro	Thr	Phe	Glu	Ser	Ser	Ser
						225				230					240
Asn	Ser	Leu	Thr	Val	Val	Leu	Ser	Thr	Asp	Tyr	Ala	Asn	Ser	Tyr	Arg
						245				250					255
Gly	Phe	Ser	Ala	Ser	Tyr	Thr	Ser	Ile	Tyr	Ala	Glu	Asn	Ile	Asn	Thr
						260				265					270
Thr	Ser	Leu	Thr	Cys	Ser	Ser	Asp	Arg	Met	Arg	Val	Ile	Ile	Ser	Lys
						275				280					285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
 290 295 300

Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val  
 305 310 315 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335

Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
 340 345 350

Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
 355 360 365

His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380

Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
 420 425 430

Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
 435 440 445

Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu  
 485 490 495

Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510

Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525

Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540

Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

<p>565</p> <p>Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe 580                       585                       590</p> <p>Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr 595                       600                       605</p> <p>&lt;210&gt; 191</p> <p>&lt;211&gt; 21</p> <p>&lt;212&gt; DNA</p> <p>&lt;213&gt; Artificial Sequence</p> <p>&lt;220&gt;</p> <p>&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe</p> <p>&lt;400&gt; 191</p> <p>tctctattcc aaactgtggc g</p> <p>&lt;210&gt; 192</p> <p>&lt;211&gt; 22</p> <p>&lt;212&gt; DNA</p> <p>&lt;213&gt; Artificial Sequence</p> <p>&lt;220&gt;</p> <p>&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe</p> <p>&lt;400&gt; 192</p> <p>tttgatgacg attcgaagg t</p> <p>&lt;210&gt; 193</p> <p>&lt;211&gt; 47</p> <p>&lt;212&gt; DNA</p> <p>&lt;213&gt; Artificial Sequence</p> <p>&lt;220&gt;</p> <p>&lt;223&gt; Description of Artificial Sequence: Synthetic oligonucleotide probe</p> <p>&lt;400&gt; 193</p> <p>ggaaggatcc ttcaccagcc ccaattaccc aaagccgcatt cctgagc</p> <p>&lt;210&gt; 194</p> <p>&lt;211&gt; 2362</p> <p>&lt;212&gt; DNA</p> <p>&lt;213&gt; Homo sapiens</p> <p>&lt;400&gt; 194</p> <p>gacgaaagaa cagcgctccc gagggccggg gagcctgcag agaggacagc cggcctgcgc 60 cgggacatgc ggccccagga gctccccagg ctcgcgttcc cggtgctgtct gttgctgttgc 120 ctgctgctgc cgccgcccgttcc cacagcgcca cgcgcgttca ccccacctgg 180</p>	<p>570</p> <p>575</p> <p>21</p> <p>22</p> <p>47</p>
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gagtcctgg acgcccgcga gctgcccgcg tggtttgcacc aggccaagtt cggcatctc 240  
 atccactggg gagtgtttc cgtgcccagc ttccggtagcg agtgttctg gtggtatgg 300  
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 taaaactcatt gtgcaatgt aa 2362

&lt;210&gt; 195

&lt;211&gt; 467

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

Met	Arg	Pro	Gln	Glu	Leu	Pro	Arg	Leu	Ala	Phe	Pro	Leu	Leu	Leu
1														15

Leu	Leu	Leu	Leu	Leu	Pro	Pro	Pro	Pro	Cys	Pro	Ala	His	Ser	Ala	Thr	
														20	25	30

Arg	Phe	Asp	Pro	Thr	Trp	Glu	Ser	Leu	Asp	Ala	Arg	Gln	Leu	Pro	Ala	
														35	40	45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe  
 50 55 60  
 Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys  
 65 70 75 80  
 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
 85 90 95  
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
 100 105 110  
 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
 115 120 125  
 Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser  
 130 135 140  
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
 145 150 155 160  
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
 165 170 175  
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
 180 185 190  
 Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
 195 200 205  
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
 210 215 220  
 Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser  
 225 230 235 240  
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
 245 250 255  
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270  
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285  
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300  
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320  
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
 370                    375                    380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
                   435                   440                   445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
· 450 · 455 · 460

Asn Val Ile  
465

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<210> 196
<211> 23
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 196  
tggtttgacc aggccaaagt t cgg

<210> 197

<212> DNA  
<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 197  
ggattcatcc tcaaggaaga gcgg 24

<210> 198

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 198
      aacttgcagc atcagccact ctgc          24

<210> 199
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 199
      ttccgtgccc agttcggtt gcgagtggat tggca          45

<210> 200
<211> 2372
<212> DNA
<213> Homo sapiens

<400> 200
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      catctgagggt gttccctgg ctctgaaggg gttaggcacga tggccagggtg cttcagcctg 180
      gtgttgcttc tcacttccat ctggaccacg aggctctgg tccaaaggctc tttgcgtgca 240
      gaagagcttt ccatccaggt gtcatgcaga attatggggta tcacccttgt gagcaaaaag 300
      gcgaaccagc agctgaattt cacagaagct aaggaggcgt gttaggtgtc gggactaagt 360
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      tggttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaaa 600
      gatccccatat tcaacactca aactgcaaca caaaacaacag aatttattgt cagtgacagt 660
      acctactcggtt tggcatcccc ttactctaca atacctggcc ctactactac tcctctgtc 720
      ccagcttcca ctcttattcc acggagaaaa aaattgattt gtgtcacaga agttttatg 780
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caaatgtatc actagccctc cttttccaa caagaaggga ctgagagatg cagaaatatt 2340  
tgtgacaaaaa aattaaagca ttttagaaaaac tt 2372

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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1				5					10						15

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile  
20 25 30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala  
35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu  
50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala  
65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val  
85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly  
100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys  
115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile  
 130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 202  
 gagcttcca tccaggtgtc atgc

24

<210> 203  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 203  
gtcagtgaca gtacctactc gg

22

<210> 204  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 204  
tggagcagga ggagtagtag tagg

24

<210> 205  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 205  
aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206  
<211> 1620  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (973)  
<223> a, t, c or g

<220>  
<221> modified\_base  
<222> (977)  
<223> a, t, c or g

<220>  
<221> modified\_base  
<222> (996)  
<223> a, t, c or g

<220>  
<221> modified\_base

<222> (1003)

<223> a, t, c or q

<400> 206

agatggcggt cttggcacct ctaattgctc tcgtgtattc ggtgcgcgca cttcacat 60  
ggctcgccca accttactac cttctgtcgg ccctgtctc tgctgccttc ctactcgtga 120  
ggaaaactgcc gcccgtctgc cacggctgtc ccacccaacg cgaagacggt aaccctgtg 180  
actttgactg gagagaagtg gagatctga ttttctca gtgccattgtg atgatgaaga 240  
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<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg  
1 5 10 15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu  
20 25 30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly  
35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg  
50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn  
65 70 75 80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
 85 90 95  
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
 100 105 110  
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
 115 120 125  
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
 130 135 140  
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
 145 150 155 160  
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
 165 170 175  
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
 180 185 190  
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
 195 200 205  
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
 210 215 220  
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
 225 230 235 240  
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
 245 250 255  
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
 260 265 270  
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
 275 280 285  
 Asp Gly Glu Asn Lys Lys Asp Lys  
 290 295  
 <210> 208  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
 <400> 208  
 gcttggatata tcgcacatgggc ctac

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg 24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
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 cccattgctc ctgctgcccg gtcctacgg actgcccttc tacaacggct tctactactc 180  
 caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240  
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 tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540  
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 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1920  
 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1980  
 aaaaaa 1985

&lt;210&gt; 213

&lt;211&gt; 360

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 213

Met	Gly	Leu	Leu	Leu	Leu	Val	Pro	Leu	Leu	Leu	Pro	Gly	Ser	Tyr
1								10					15	

Gly	Leu	Pro	Phe	Tyr	Asn	Gly	Phe	Tyr	Tyr	Ser	Asn	Ser	Ala	Asn	Asp
								20					30		

Gln	Asn	Leu	Gly	Asn	Gly	His	Gly	Lys	Asp	Leu	Leu	Asn	Gly	Val	Lys
								35					45		

Leu	Val	Val	Glu	Thr	Pro	Glu	Glu	Thr	Leu	Phe	Thr	Tyr	Gln	Gly	Ala
								50				60			

Ser	Val	Ile	Leu	Pro	Cys	Arg	Tyr	Arg	Tyr	Glu	Pro	Ala	Leu	Val	Ser
								65					80		

Pro	Arg	Arg	Val	Arg	Val	Lys	Trp	Trp	Lys	Leu	Ser	Glu	Asn	Gly	Ala
								85					95		

Pro	Glu	Lys	Asp	Val	Leu	Val	Ala	Ile	Gly	Leu	Arg	His	Arg	Ser	Phe
								100					110		

Gly	Asp	Tyr	Gln	Gly	Arg	Val	His	Leu	Arg	Gln	Asp	Lys	Glu	His	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125
Val Ser Leu Glu Ile Gln Asp	Leu Arg Leu Glu Asp	Tyr Gly Arg Tyr
130	135	140
Arg Cys Glu Val Ile Asp	Gly Leu Glu Asp	Glu Ser Gly Leu Val Glu
145	150	155
Leu Glu Leu Arg Gly Val Val Phe Pro	Tyr Gln Ser Pro Asn Gly Arg	
165	170	175
Tyr Gln Phe Asn Phe His Glu Gly	Gln Gln Val Cys Ala Glu Gln Ala	
180	185	190
Ala Val Val Ala Ser Phe Glu Gln	Leu Phe Arg Ala Trp Glu Glu Gly	
195	200	205
Leu Asp Trp Cys Asn Ala Gly	Trp Leu Gln Asp Ala Thr Val Gln Tyr	
210	215	220
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly	Gly Pro Gly Leu Ala Pro	
225	230	235
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg	Leu His Arg Tyr Asp	
245	250	255
Val Phe Cys Phe Ala Thr Ala Leu Lys	Gly Arg Val Tyr Tyr Leu Glu	
260	265	270
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu	Ala Cys Gln Glu	
275	280	285
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe	Ala Ala Trp Lys	
290	295	300
Phe His Gly Leu Asp Arg Cys Asp Ala Gly	Trp Leu Ala Asp Gly Ser	
305	310	315
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys	Gly Pro Pro Glu	
325	330	335
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser	Arg Leu Tyr	
340	345	350
Gly Val Tyr Cys Tyr Arg Gln His		
355	360	
<210> 214		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215

ttcccttgtg ggttggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217

agccagttag gaaatgcg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218

tgtccaaagt acacacacacct gagg

24



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Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly			
20	25	30	
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala			
35	40	45	
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val			
50	55	60	
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu			
65	70	75	80
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp			
85	90	95	
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg			
100	105	110	
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp			
115	120	125	
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly			
130	135	140	
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr			
145	150	155	160
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp			
165	170	175	
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu			
180	185	190	
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr			
195	200	205	
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu			
210	215	220	
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala			
225	230	235	240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn			
245	250	255	
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro			
260	265	270	
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu			
275	280	285	

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 225  
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 <210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens  
 <400> 226  
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<212> PRT

<213> Homo sapiens

<400> 227

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Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro  
85 90 95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln  
           100                 105                 110

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195 200 205

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 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
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 Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495  
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
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 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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<400> 228

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18

<210> 229

<211> 18

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<220>

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<400> 229

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18

<210> 230

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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18

<210> 231

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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18

<210> 232

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&lt;210&gt; 236

&lt;211&gt; 350

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 236

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Lys	Pro	Gly	Pro	Ala	Leu	Ser	Tyr	Pro	Gln	Glu	Glu	Ala	Thr	Leu	Asn
								35		40			45		

Glu	Met	Phe	Arg	Glu	Val	Glu	Glu	Leu	Met	Glu	Asp	Thr	Gln	His	Lys
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Leu	Arg	Ser	Ala	Val	Glu	Glu	Met	Glu	Ala	Glu	Glu	Ala	Ala	Lys
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 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
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<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser  
35 40 45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu  
50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu  
65 70 75

Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly  
80 85 90

Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe  
95 100 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu  
110 115 120

Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His  
125 130 135

Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His  
140 145 150

Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser  
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 Asn Leu Leu Arg Leu His Leu Asn Ser Asn Leu Leu Arg Ala Ile  
                   170                  175                  180  
 Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met  
                   185                  190                  195  
 Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg  
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 Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu  
                   215                  220                  225  
 Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu  
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 Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg  
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 Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys  
                   260                  265                  270  
 Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu  
                   275                  280                  285  
 His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser  
                   290                  295                  300  
 Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu  
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 Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala  
                   320                  325                  330  
 Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn  
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 Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys  
                   365                  370                  375  
 Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile  
                   380                  385                  390  
 Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg  
                   395                  400                  405  
 Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys

410	415	420
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425	430	435
Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu		
440	445	450
Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu		
455	460	465
Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly		
470	475	480
Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr		
485	490	495
Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val		
500	505	510
Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu		
515	520	525
Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His		
530	535	540
Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn		
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Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr		
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Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr		
575	580	585
Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala		
590	595	600
Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr		
605	610	615
Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly		
620	625	630
Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly		
635	640	645
Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly		
650	655	660
Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser		
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Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
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Leu Pro Pro Leu Ser Gln Asn Ser  
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<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

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<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

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<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

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<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

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catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200  
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 a 3401  
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 <213> Homo Sapien  
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 Cys Thr Val Asp Ile Glu Ser Leu Thr Gly Tyr Arg Thr Tyr Arg  
 35 40 45  
 Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe  
 50 55 60  
 Tyr Ile Ser Leu Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr  
 65 70 75  
 Leu Trp Trp Met Leu Arg Arg Ser Leu Lys Lys Tyr Ser Phe Glu  
 80 85 90  
 Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

95	100	105
Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro		
110	115	120
Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu		
125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Glu Trp Thr Leu Asp		
140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu		
155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp		
170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val		
185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu		
200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala		
215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp		
230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu		
245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr		
260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu		
275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp		
290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr		
305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr		
320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser		
335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn		
350	355	360

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His
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														365
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
														390
														380
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
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														395
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
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														410
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
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														425
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
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														440
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
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														455
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
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Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
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Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
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														500
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
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														515
Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
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														530
Ala	Asp	Lys	Glu	Gln	Ala									
														545

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&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 251

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&lt;210&gt; 252

&lt;211&gt; 24

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<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 252
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<210> 253
<211> 47
<212> DNA
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<220>
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<400> 253
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<210> 254
<211> 1650
<212> DNA
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tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200
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               20                 25                     30  
 Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val  
               35                 40                     45

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Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln
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Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu
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Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp
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Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr
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Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu
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Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe
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Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu
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Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly
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Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu
					200					205				210
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys
					215					220				225
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala
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Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr
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Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser
					275					280				285
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His
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Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly

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Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp 320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe 335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly 350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp 365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu 380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp 395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn 410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser 425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln 440	445	450
Gln Glu		

&lt;210&gt; 256

&lt;211&gt; 1100

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 256

ggccgcggga gaggaggcca tggcgcgcg cggggcgctg ctgctggcgc 50

tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100

ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150

tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200

tgtggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctggca 250

ctcacggcgg cgcaactgctt tgaaacctat agtgcaccta gtgatccctc 300

cgggtggatg gtccagttg gccagctgac ttccatgcca tccttctgga 350

gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

cctcgctacc tgggaaattc accctatgac attgccttgg tgaagctgtc 450  
 tgcacctgtc acctacacta aacacatcca gccccatctgt ctccaggcct 500  
 ccacattga gtttgagaac cggacagact gatgggtgac tggctggggg 550  
 tacatcaaag aggatgaggc actgccatct cccccacaccc tccaggaagt 600  
 tcaggtcgcc atcataaaca actctatgtg caaccacactc ttctcaagt 650  
 acagttccg caaggacatc tttggagaca tggtttgtc tggcaacgcc 700  
 caaggcggga aggatgcctg cttcggtgac tcaggtggac ccttggcctg 750  
 taacaagaat ggactgtggt atcagattgg agtcgtgagc tggggagtgg 800  
 gctgtggtcg gcccaatcgg cccgggtgtct acaccaatat cagccaccac 850  
 tttgagtgga tccagaagct gatggcccag agtggcatgt cccagccaga 900  
 cccctcctgg ccactactct ttttccctct tctctgggt ctcccactcc 950  
 tggggccgggt ctgagcctac ctgagcccat gcagcctggg gccactgcca 1000  
 agtcaggccc tggttctttt ctgtcttggt tggtaataaa cacattccag 1050  
 ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100  
 <210> 257  
 <211> 314  
 <212> PRT  
 <213> Homo Sapien  
 <400> 257  
 Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg  
 1 5 10 15  
 Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser  
 20 25 30  
 Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly  
 35 40 45  
 Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg  
 50 55 60  
 Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg  
 65 70 75  
 Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu  
 80 85 90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
                  95                     100                     105  
  
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe  
                  110                     115                     120  
  
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro  
                  125                     130                     135  
  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
                  140                     145                     150  
  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
                  155                     160                     165  
  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
                  170                     175                     180  
  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
                  185                     190                     195  
  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
                  200                     205                     210  
  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
                  215                     220                     225  
  
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
                  230                     235                     240  
  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
                  245                     250                     255  
  
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
                  260                     265                     270  
  
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
                  275                     280                     285  
  
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu  
                  290                     295                     300  
  
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val  
                  305                     310

<210> 258  
 <211> 2427  
 <212> DNA  
 <213> Homo Sapien

<400> 258  
 cccacgcgtc cgccggacgacg tgggaaggac agaatggac tccaaggctg 50

cctcctaggg ctctttgccccc tcatcccttc tggcaaatgc agttacagcc 100  
cgaggccccga ccagcggagg acgctgcccc caggctgggt gtcctgggc 150  
cgtgcggacc ctgaggaaga gctgagtctc acctttgccccc tgagacagca 200  
gaatgtggaa agactctcg agctggtgca ggctgtgtcg gatcccagct 250  
cteccaata cgaaaaatac ctgaccctag agaatgtggc tgatctggtg 300  
aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggcagc 350  
cgagccccag aagtgccatt ctgtgatcac acaggacttt ctgacttgct 400  
ggctgagcat ccgacaagca gagctgctgc tccctggggc tgagttcat 450  
cactatgtgg gaggacctac ggaaacccat gttgtaaggt ccccacatcc 500  
ctaccagctt ccacaggcct tggcccccata tgtggacttt gtggggggac 550  
tgcaccgttt tcccccaaca tcattccctga ggcaacgtcc tgagccgcag 600  
gtgacagggga ctgtaggcct gcatctgggg gtaacccctt ctgtgatccg 650  
taagcgatac aacttgacct cacaagacgt gggctctggc accagcaata 700  
acagccaagc ctgtgcccag ttccctggagc agtatttcca tgactcagac 750  
ctggctcagt tcattcccttc ctccgggtggc aactttgcac atcaggcatc 800  
agtagcccgat gtgggttgac aacagggccg gggccggggcc gggattgagg 850  
ccagtctaga tgtgcagttac ctgatgagtg ctgggtccaa catctccacc 900  
tgggtctaca gtagccctgg ccggcatgag ggacaggagc cttccctgca 950  
gtggctcatg ctgctcagta atgagtca cctgccacat gtgcatactg 1000  
tgagctatgg agatgatgag gactccctca gcagcgccta catccagcgg 1050  
gtcaacactg agctcatgaa ggctgccgtc cggggctctca ccctgcttt 1100  
cgccctcaggt gacagtgggg ccgggtgttg gtctgtctct ggaagacacc 1150  
agttccggccc taccccttc gcctccagcc cctatgtcac cacagtggga 1200  
ggcacatcct tccaggaacc tttccctcatc acaaataaaa ttgttgacta 1250  
tatcagtgggt ggtggcttca gcaatgtgtt cccacggcct tcataccagg 1300  
aggaagctgt aacgaagttc ctgagctcta gccccccaccc gccaccatcc 1350  
agttacttca atgccagtgcc cggtgcctac ccagatgtgg ctgcactttc 1400

tgatggctac tgggtggtca gcaacagagt gcccattcca tgggtgtccg 1450  
 gaacctcgga ctctactcca gtgtttgggg ggatcctata cttgatcaat 1500  
 gagcacagga tccttagtgg ccgcggccct cttggcttc tcaacccaag 1550  
 gctctaccag cagcatgggg caggtctt tt tgatgtaacc cgtggctgcc 1600  
 atgagtcctg tctggatgaa gaggttagagg gccagggttt ctgctctgg 1650  
 cctggctggg atcctgtaac aggctggga acaccaactt cccagcttg 1700  
 ctgaagactc tactcaaccc ctgacccttt cctatcagga gagatggctt 1750  
 gtccccgtcc ctgaagctgg cagttcagtc ccttattctg ccctgttgaa 1800  
 agccctgctg aaccctcaac tattgactgc tgcagacagc ttatctccct 1850  
 aaccctgaaa tgctgtgagc ttgacttgac tcccaaccct accatgctcc 1900  
 atcatactca ggtctcccta ctcctgcctt agattcctca ataagatgct 1950  
 gtaactagca tttttgaat gcctctccct ccgcattctca tctttctt 2000  
 ttcaatcagg cttttccaaa ggggtgtata cagactctgt gcactatttc 2050  
 acttgatatt cattcccaa ttcaactgcaa ggagacctct actgtcaccg 2100  
 tttactctt cctaccctga catccagaaa caatggcctc cagtcatac 2150  
 ttctcaatct ttgctttatg gccttccat catagttgcc cactccctct 2200  
 ccttacttag cttccaggc ttaacttctc tgactactct tgtcttcctc 2250  
 tctcatcaat ttctgcttct tcattggatg ctgacccctca ttgctccatt 2300  
 ttagatattt tgctcttctc agttactca ttgtccctg gaacaaatca 2350  
 ctgacatcta caaccattac catctacta aataagactt tctatccaat 2400  
 aatgattgat acctcaaatg taaaaaa 2427

&lt;210&gt; 259

&lt;211&gt; 556

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 259

Met	Gly	Leu	Gln
1	5	10	15

Ser	Gly	Lys	Cys
Ser	Tyr	Pro	Glu

20	25	30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu		
35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly		
290	295	300
Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser		
305	310	315
Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp		
320	325	330
Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met		
335	340	345
Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp		
350	355	360
Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg		
365	370	375
Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly		
380	385	390
Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp		
395	400	405
Tyr Ile Ser Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser		
410	415	420
Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His		
425	430	435
Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro		
440	445	450
Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg		
455	460	465
Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val		
470	475	480
Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser		
485	490	495
Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln		
500	505	510
His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser		
515	520	525
Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro		
530	535	540
Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu		
545	550	555

## Cys

<210> 260  
 <211> 1638  
 <212> DNA  
 <213> Homo Sapien

<400> 260  
 gccgcgcgct ctctccggc gcccacacct gtctgagcgg cgca gcgagc 50  
 cggggccgg ggcccgtgct cggcgccgaa cagt gctcggtatggcagg 100  
 attccagggc tccttcttcct tctttttt ctgctctgtg ctgttggca 150  
 agtgagccct tacagtgc cctggaaacc cacttggcct gcataccgccc 200  
 tccctgtcgt cttggccctca attagccaa gccagacttt 250  
 ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300  
 taaggaaact ccactgccc cttacgaaga ggccaagcaa tatctgtctt 350  
 atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcattc 400  
 tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450  
 ttcaggaaag tctcgaagga agccggcagat ttatggctat gacagcagg 500  
 tcagcattt tgggaaggac ttccctgctca actaccctt ctaacatca 550  
 gtgaagttat ccacgggctg caccggcacc ctgggtggcag agaagcatgt 600  
 cctcacagct gcccactgca tacacgatgg aaaaacctat gtgaaaggaa 650  
 cccagaagct tcgagtgccc ttccctaaagc ccaagttaa agatgggt 700  
 cgaggggcca acgactccac ttccatgtc cccgagcaga tgaaatttca 750  
 gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaaggc 800  
 atgccaatga catcgccatg gattatgatt atgcccctt ggaactcaaa 850  
 aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctcctgctaa 900  
 gcagctgcca gggggcagaa ttccatgtc tggttatgac aatgaccgac 950  
 caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000  
 ttgctctacc agcaatgcga tgcccagcca ggggcccagcg ggtctgggt 1050  
 ctatgtgagg atgtggaaga gacagcagca gaagtggag cgaaaaatta 1100

ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150  
gatttcaacg tggctgtcag aatcactcct ctcaaataatg cccagattg 1200  
ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250  
ttccctcctg gcagcaatta agggtcttca tgttcttatt ttaggagagg 1300  
ccaaattgtt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350  
tgtgtgtaaag gtgtcttata atctttacc tatttcttac aattgcaaga 1400  
tgactggctt tactatttga aaactggttt gtgtatcata tcataatatca 1450  
tttaaggcagt ttgaaggcat acttttgcattt agaaaataaaaa aaaataactga 1500  
tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgttttg 1550  
caaactttga ttttatttc atctgaactt gtttcaaaga tttatattaa 1600  
atatttqqca tacaagagat atgaaaaaaaaaaa aaaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu  
                   1                     5                         10                     15

Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro  
20 25 30

Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr  
35 40 45

Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu  
50 55 60

Val Ser Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu  
65 70 75

Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu  
80 85 90

Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile

Leu Ser Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser  
116 117 118 119 120



<210> 262  
<211> 1378  
<212> DNA  
<213> Homo Sapien  
  
<400> 262  
gcatcgccct gggtctctcg agcctgctgc ctgctccccc gccccaccag 50  
ccatggtggt ttctggagcg ccccccagccc tgggtggggg ctgtctcggc 100  
accttcacct ccctgctgtc gctggcgctcg acagccatcc tcaatgcggc 150  
caggataacct gttcccccag cctgtggaa gccccagcag ctgaaccggg 200  
ttgtggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250  
atccagaaga atgggaccca ccactgcgca ggttctctgc tcaccagccg 300  
ctgggtgatc actgctgcc actgtttcaa ggacaacctg aacaaaccat 350  
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400  
cggtcccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450  
ctggaaggaa ggtgcctgtg cagacattgc cctggtgctg ctgcagcgct 500  
ccatacagtt ctcagagcgg gtcctgccc tctgcctacc tgatgcctct 550  
atccacactcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600  
ccaagatgga gttccctgc cccaccctca gaccctgcag aagctgaagg 650  
ttccttatcat cgactcgaa gtctgcagcc atctgtactg gcggggagca 700  
ggacagggac ccatcactga ggacatgctg tgtgccggct acttggaggg 750  
ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800  
tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850  
gccgagcgca acaggcccgg ggtctacatc agcctctctg cgccaccgctc 900  
ctgggtggag aagatcgtgc aagggtgtca gtcggcgccc cgcgctcagg 950  
gggggtggggc cctcaggcga ccgagccagg gtcctggggc cgccgcgcgc 1000  
tccttagggcg cagcgggacg cggggctcg atctgaaagg cgccagatc 1050  
cacatctgga tctggatctg cggcgccctc gggcggttc ccccgccgta 1100  
aataggctca tctacactcta cctctggggg cccggacggc tgctgcggaa 1150

aggaaacccc ctcgggacc cgccccacgg cctcaggccc ccctccaagg 1200  
catcaggccc cgcccaacgg cctcatgtcc ccggggccac gacttccggc 1250  
cccgcccccg ggccccagcg cttttgtgtataaatgtt aatgattttt 1300  
ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350  
ataaaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu  
1 5 10 15

Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu  
20 25 30

Asn Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln  
35 40 45

Gln Leu Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu  
50 55 60

Trp Pro Trp Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys  
65 70 75

Ala Gly Ser Leu Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His  
80 85 90

Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu  
95 100 105

Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser Gln Lys  
110 115 120

Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys  
125 130 135

Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser  
149 150 151 152 153 154 155 156

Ile Gln Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala

Ser Ile His Leu Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu  
                  185                     190                 195  
 Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His  
                  200                     205                 210  
 Leu Tyr Trp Arg Gly Ala Gly Pro Ile Thr Glu Asp Met  
                  215                     220                 225  
 Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly  
                  230                     235                 240  
 Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu  
                  245                     250                 255  
 Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn  
                  260                     265                 270  
 Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val  
                  275                     280                 285  
 Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly  
                  290                     295                 300  
 Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala  
                  305                     310                 315

Arg Ser

<210> 264  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264  
 gtccgcaagg atgcctacat gttc 24

<210> 265  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 265  
 gcagaggtgt ctaaggttg 19

<210> 266  
 <211> 24

<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 266  
agctctagac caatgccagc ttcc 24  
  
<210> 267  
<211> 45  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 267  
gccaccaact cctgcaagaa ctttcagaa ctgcccctgg tcattg 45  
  
<210> 268  
<211> 25  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 268  
ggggaaattca cccttatgaca ttgcc 25  
  
<210> 269  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 269  
gaatgccctg caagcatcaa ctgg 24  
  
<210> 270  
<211> 50  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic Oligonucleotide Probe  
  
<400> 270  
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 271  
gcggaagggc agaatgggac tccaaag 26

<210> 272  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 272  
cagccctgcc acatgtgc 18

<210> 273  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 273  
tactgggtgg tcagcaac 18

<210> 274  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 274  
ggcgaagagc agggtgagac cccg 24

<210> 275  
<211> 45

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 275  
gccctcatcc tctctggcaa atgcagttac agcccgagc ccgac 45

<210> 276  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 276  
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<210> 277  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 277  
ggctatgaca gcaggttc 18

<210> 278  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 278  
tgacaatgac cgaccagg 18

<210> 279  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic Oligonucleotide Probe

<400> 279  
gcatcgatt gctggtagag caag 24

<210> 280  
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<212> DNA  
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<220>

<223> Synthetic Oligonucleotide Probe

<400> 280  
ttacagtgcc ccctggaaac ccacttggcc tgcataaccgc ctccc 45

<210> 281  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281  
cgtctcgagc gtcataaca gttccattgc ccca 34

<210> 282  
<211> 61  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282  
tggaggggga gcgggatgct tgtctggcg actccggggg cccccatg 50  
tgccaggtgg a 61

<210> 283  
<211> 119  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283  
ccctcagacc ctgcagaagc tgaagggtcc tatcatcgac tcgaaatct 50  
gcagccatct gtactggcg ggagcaggac agggaccat cactgaggac 100  
atgctgttg ccggctact 119

<210> 284  
<211> 1875  
<212> DNA  
<213> Homo Sapien

<400> 284  
gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50  
ccgctactgc tactgcttgt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgttga tggtgagct gcacaacctc tacccggccc 150  
aggatatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200  
ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt gggccacaa 250  
caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300  
gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350  
tacaacctca gcgccgcccc ctgcagccca ggccagatgt gcggccacta 400  
cacgcaggtg gtatggcca agacagagag gatcggctgt gttcccact 450  
tctgtgagaa gctccaggggt gttgaggaga ccaacatcga attactggtg 500  
tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550  
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tctgtgaacc catcggaagc ccggaagatg ctcaggattt gccttacctg 650  
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caagcctagc gttgtgtcag ggctgaactc gggccctggc catgtgtggg 1350  
gccctctccct gggactactg ctctgcctc ctctggtgtt ggctggaatc 1400

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 ggccctccgg aagggaaagg ctacggggca tgtgcctcat cacaccatcc 1550  
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 tgcccacaca gcatgtgcgc tctccctgag tgcctgtgta gctggggatg 1750  
 gggattccta gggcagatg aaggacaagc cccactggag tggggtttt 1800  
 tgagtgggg aggcaaggac gagggaaagga aagtaactcc tgactctcca 1850  
 ataaaaaacct gtccaacctg tgaaa 1875

&lt;210&gt; 285

&lt;211&gt; 463

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 285

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1	5	10	15		
Leu Leu Leu Val Ala Thr Thr Gly Pro Val Gly Ala Leu Thr Asp					
	20	25	30		
Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala					
	35	40	45		
Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp					
	50	55	60		
Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val					
	65	70	75		
Trp Gly His Asn Lys Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe					
	80	85	90		
Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu					
	95	100	105		
Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys					
	110	115	120		
Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala					
	125	130	135		

Lys	Thr	Glu	Arg	Ile	Gly	Cys	Gly	Ser	His	Phe	Cys	Glu	Lys	Leu
				140					145					150
Gln	Gly	Val	Glu	Glu	Thr	Asn	Ile	Glu	Leu	Leu	Val	Cys	Asn	Tyr
				155				160						165
Glu	Pro	Pro	Gly	Asn	Val	Lys	Gly	Lys	Arg	Pro	Tyr	Gln	Glu	Gly
				170				175						180
Thr	Pro	Cys	Ser	Gln	Cys	Pro	Ser	Gly	Tyr	His	Cys	Lys	Asn	Ser
				185				190						195
Leu	Cys	Glu	Pro	Ile	Gly	Ser	Pro	Glu	Asp	Ala	Gln	Asp	Leu	Pro
				200				205						210
Tyr	Leu	Val	Thr	Glu	Ala	Pro	Ser	Phe	Arg	Ala	Thr	Glu	Ala	Ser
				215				220						225
Asp	Ser	Arg	Lys	Met	Gly	Thr	Pro	Ser	Ser	Leu	Ala	Thr	Gly	Ile
				230				235						240
Pro	Ala	Phe	Leu	Val	Thr	Glu	Val	Ser	Gly	Ser	Leu	Ala	Thr	Lys
				245				250						255
Ala	Leu	Pro	Ala	Val	Glu	Thr	Gln	Ala	Pro	Thr	Ser	Leu	Ala	Thr
				260				265						270
Lys	Asp	Pro	Pro	Ser	Met	Ala	Thr	Glu	Ala	Pro	Pro	Cys	Val	Thr
				275				280						285
Thr	Glu	Val	Pro	Ser	Ile	Leu	Ala	Ala	His	Ser	Leu	Pro	Ser	Leu
				290				295						300
Asp	Glu	Glu	Pro	Val	Thr	Phe	Pro	Lys	Ser	Thr	His	Val	Pro	Ile
				305				310						315
Pro	Lys	Ser	Ala	Asp	Lys	Val	Thr	Asp	Lys	Thr	Lys	Val	Pro	Ser
				320				325						330
Arg	Ser	Pro	Glu	Asn	Ser	Leu	Asp	Pro	Lys	Met	Ser	Leu	Thr	Gly
				335				340						345
Ala	Arg	Glu	Leu	Leu	Pro	His	Ala	Gln	Glu	Glu	Ala	Glu	Ala	Glu
				350				355						360
Ala	Glu	Leu	Pro	Pro	Ser	Ser	Glu	Val	Leu	Ala	Ser	Val	Phe	Pro
				365				370						375
Ala	Gln	Asp	Lys	Pro	Gly	Glu	Leu	Gln	Ala	Thr	Leu	Asp	His	Thr
				380				385						390
Gly	His	Thr	Ser	Ser	Lys	Ser	Leu	Pro	Asn	Phe	Pro	Asn	Thr	Ser
				395				400						405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

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caaggcaagt tccatgagcc accttcaaag cttcgagaa gtgaaaactga 200  
acaacaatga attggagacc attccaaatc tgggaccagt ctggcaaat 250  
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atatttcaga gctccaaact gcatttccag ccctacagct caaatatctg 400  
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tttggccaac acactccttg tgttaaagct gaacaggaac cgaatctcag 500  
ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattt 550  
aaccgaaaca agattaaaaa ttagatgga ctgacattcc aaggcattgg 600  
tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650  
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cctgggagtt ctgccagaag ctcagtgagc tggacctaac tttcaatcac 850  
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actgcacatt gggacaaca gagtcagcta cattgctgat tgccttcc 950  
gggggcttcc cagttaaag actttggatc tgaagaacaa tggaaatttcc 1000  
tggactattt aagacatgaa tgggttcc tctggcttg acaaactgag 1050  
gcgactgata ctccaaggaa atcgatccg ttcttattact aaaaaagcct 1100  
tcactggttt ggtatgcattt gagcatctag acctgagtgaa caacgcaatc 1150  
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cacagtgggt ggccggaaaac aactttcaga gctttgtaaa tgcagttgt 1300  
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 taaatcatga ttatttatg tattttata atgccagatt tctttttag 3550  
 gaaaatgagt tactaaagca ttttaataa tacctgcctt gtaccatttt 3600  
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 tgtcaatttg aa 3662

<210> 290  
 <211> 1059  
 <212> PRT  
 <213> Homo Sapien

<400> 290  
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 Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
 20 25 30

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
                  35                        40                        45  
 Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
                  50                        55                        60  
 Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
                  65                        70                        75  
 Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
                  80                        85                        90  
 Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
                  95                        100                      105  
 Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
                  110                       115                      120  
 Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
                  125                       130                      135  
 Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
                  140                       145                      150  
 Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn  
                  155                       160                      165  
 Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala  
                  170                       175                      180  
 Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met  
                  185                       190                      195  
 Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu  
                  200                       205                      210  
 Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly  
                  215                       220                      225  
 Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn  
                  230                       235                      240  
 Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu  
                  245                       250                      255  
 Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser  
                  260                       265                      270  
 Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn  
                  275                       280                      285  
 Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser

290	295	300
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
305	310	315
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
455	460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu		
500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
530	535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
545	550	555

Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro  
 560 565 570  
 Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro  
 575 580 585  
 Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val  
 590 595 600  
 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser  
 605 610 615  
 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr  
 620 625 630  
 Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp  
 635 640 645  
 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala  
 650 655 660  
 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser  
 665 670 675  
 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln  
 680 685 690  
 Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr  
 695 700 705  
 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val  
 710 715 720  
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met  
 725 730 735  
 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val  
 740 745 750  
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val  
 755 760 765  
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Asn Glu Asp Cys  
 770 775 780  
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
 785 790 795  
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly  
 800 805 810

Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser
				815						820				825
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr
				830					835					840
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr
				845					850					855
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr
				860					865					870
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His
				875					880					885
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr
				890					895					900
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His
				905					910					915
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp
				920					925					930
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn
				935					940					945
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu
				950					955					960
Asp	Phe	Ser	Ala	Asn	Pro	Glu	Pro	Ala	Ser	Val	Ala	Ser	Ser	Asn
				965					970					975
Ser	Phe	Met	Gly	Thr	Phe	Gly	Lys	Ala	Leu	Arg	Arg	Pro	His	Leu
				980					985					990
Asp	Ala	Tyr	Ser	Ser	Phe	Gly	Gln	Pro	Ser	Asp	Cys	Gln	Pro	Arg
				995					1000					1005
Ala	Phe	Tyr	Leu	Lys	Ala	His	Ser	Ser	Pro	Asp	Leu	Asp	Ser	Gly
				1010					1015					1020
Ser	Glu	Glu	Asp	Gly	Lys	Glu	Arg	Thr	Asp	Phe	Gln	Glu	Glu	Asn
				1025					1030					1035
His	Ile	Cys	Thr	Phe	Lys	Gln	Thr	Leu	Glu	Asn	Tyr	Arg	Thr	Pro
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				1055										
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&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

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<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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20 25 30

Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln  
35 40 45

Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val  
50 55 60

Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser  
65 70 75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile  
                   80                   85                   90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu  
95 100 105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe  
110 115 120

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg  
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Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu  
140 145 150

Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser

155	160	165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly		
170	175	180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly		
185	190	195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg		
200	205	210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp		
215	220	225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln		
230	235	240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile		
245	250	255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val		
260	265	270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp		
275	280	285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His		
290	295	300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp		
305	310	315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys		
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Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp		
335	340	345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro		
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Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys		
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Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn		
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395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp		
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 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
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 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
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 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
 575 580 585  
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
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 Tyr Lys Ser Pro Phe Asn His Thr Thr Val Asn Thr Ile Asn  
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<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

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					20				25				30	

Gly	Arg	Gly	Glu	Leu	Gly	Gln	Pro	Ser	Gly	Val	Ala	Ala	Glu	Arg
					35				40				45	

Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Leu	Gly	Asp	Leu	Leu	Asp	Cys
					50				55				60	

Ser	Arg	Lys	Arg	Leu	Ala	Arg	Leu	Pro	Glu	Pro	Leu	Pro	Ser	Trp
					65				70				75	

Val	Ala	Arg	Leu	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
					80				85				90	

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu
					95				100				105	

Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser
					110				115				120	

Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu
					125				130				135	

Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu
					140				145				150	

Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro
					155				160				165	

Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr
					170				175				180	

Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu
					185				190				195	

Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys
					200				205				210	

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

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Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met 245 250 255		
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu 260 265 270		
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly 275 280 285		
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn 290 295 300		
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu 305 310 315		
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser 320 325 330		
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn 335 340 345		
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser 350 355 360		
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile 365 370 375		
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg 380 385 390		
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala 395 400 405		
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn 410 415 420		
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys 425 430 435		
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys 440 445 450		
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln 455 460 465		
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly 470 475 480		

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
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Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
500	505	510
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
515	520	525
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
530	535	540
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
545	550	555
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu		
560	565	570
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
575	580	585
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
590	595	600
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
605	610	615
Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro		
620	625	630
Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro		
635	640	645
Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val		
650	655	660
Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser		
665	670	675
Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr		
680	685	690
Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp		
695	700	705
Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala		
710	715	720
Gly Gly Ser Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser		
725	730	735
Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln		
740	745	750

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr  
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 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val  
 770 775 780  
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met  
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 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val  
 800 805 810  
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val  
 815 820 825  
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys  
 830 835 840  
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro  
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 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly  
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 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
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 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 905 910 915  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
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 935 940 945  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 950 955 960  
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
 965 970 975  
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
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 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 995 1000 1005  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu

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1025                  1030                  1035  
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1040                  1045                  1050  
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
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Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
1070                  1075                  1080  
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
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&lt;211&gt; 509

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 315

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												20	25	30

Ser	Ser	Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys
											35	40	45	

Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys
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Gln	Pro	Arg	Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys
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Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu
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Asn	Glu	Cys	Gly	Leu	Lys	Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met
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Asn	Thr	Tyr	Gly	Ser	Tyr	Lys	Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met
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Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met
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Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val	Val	Lys	Gly	Gln	Ile	Arg
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Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg
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 ttctatcttg ttatttgtac aacaaagtaa taaggatggt tgtcacaaaa 1950  
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 aaaaaaaaaaa 2110

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<400> 320  
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 Ala Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His  
 20 25 30  
 Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe  
 35 40 45  
 His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg  
 50 55 60

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser  
       65                    70                    75  
  
 Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro  
       80                    85                    90  
  
 Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu  
       95                    100                   105  
  
 Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu  
       110                   115                   120  
  
 Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr  
       125                   130                   135  
  
 Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr  
       140                   145                   150  
  
 Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg  
       155                   160                   165  
  
 Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser  
       170                   175                   180  
  
 Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala  
       185                   190                   195  
  
 Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg  
       200                   205                   210  
  
 Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile  
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 Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu  
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 Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu  
       245                   250                   255  
  
 Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp  
       260                   265                   270  
  
 Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro  
       275                   280                   285  
  
 Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp  
       290                   295                   300  
  
 Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu  
       305                   310                   315  
  
 Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu		
440	445	450

&lt;210&gt; 321

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 321

gatcctgtca caaagccagt ggtgc 25

&lt;210&gt; 322

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 322

cactgacagg gttcctcacc cagg 24

&lt;210&gt; 323

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<213> Homo Sapien  
  
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accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggttaata 250  
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aagagtggaa gagtattgag cccgtttcat catggtttg tccaggttct 450  
gttctgatga gtagtatgtc agcactctt cagctatcta tgtggatcag 500  
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<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

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					20			25				30		

Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly
					35			40				45		

Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln
					50			55				60		

Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp
					65			70				75		

Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly
					80			85				90		

Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His
					95			100				105		

Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys
					110			115				120		

Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile
					125			130				135		

Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser
					140			145				150		

Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys
					155			160				165		

His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser
					170			175				180		

Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	Leu
					185			190				195		

Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	Ser	Lys
					200			205				210		

Arg	Arg	Arg	Pro	Gln	Pro	Tyr	Pro	Tyr	Pro	Ser	Lys	Lys	Leu	Leu
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215                    220                    225  
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu  
230                    235                    240  
Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu  
245                    250                    255  
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser  
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Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser  
275                    280  
  
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<212> DNA  
<213> Homo Sapien  
  
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<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

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Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met
				20					25					30

Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys
				35				40						45

Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
				50				55						60

Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
				65				70						75

Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
				80				85						90

Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
				95				100						105

Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
				110				115						120

Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
				125				130						135

Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
				140				145						150

Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
				155				160						165

Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
				170				175						180

Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
				185				190						195

Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Lys	Ser	Gln	Val	Leu	
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                  245                     250                     255  
  
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                  260                     265                     270  
  
 Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro  
                  275                     280                     285  
  
 Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys  
                  290                     295                     300  
  
 Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His  
                  305                     310                     315  
  
 Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu  
                  320                     325                     330  
  
 Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met  
                  335                     340                     345  
  
 Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys  
                  350                     355                     360  
  
 Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr  
                  365                     370                     375  
  
 Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp  
                  380                     385                     390  
  
 Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile  
                  395                     400                     405  
  
 Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn  
                  410                     415                     420  
  
 Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg  
                  425                     430                     435  
  
 Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala  
                  440                     445                     450  
  
 Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr  
                  455                     460                     465  
  
 Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr  
                  470                     475                     480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr  
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg  
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp  
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<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

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<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 336  
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<210> 337  
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<212> DNA  
<213> Homo Sapien

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cgactacgac tggttcttca tcatcgagga tgacacatata gtgcaggccc 900  
ccgcctggc agcccttgct ggccacctca gcatcaacca agacctgtac 950  
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tcatggggc tttggctacc ttttgtcactg gagtcctcctg cttcgtctgc 1050  
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&lt;210&gt; 339

&lt;211&gt; 772

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 339

Met	Arg	Leu	Ser	Ser	Leu	Leu	Ala	Leu	Leu	Arg	Pro	Ala	Leu	Pro
1														15

Leu	Ile	Leu	Gly	Leu	Ser	Leu	Gly	Cys	Ser	Leu	Ser	Leu	Leu	Arg
														30

Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
														45

Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
														60

Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
														75

Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
														90

Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser Thr Leu Ala Val Ala Val		
110	115	120
Asn Arg Thr Val Ala His His Phe Pro Arg Leu Leu Tyr Phe Thr		
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met Gln Val Val Ser		
140	145	150
His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser Glu Thr Leu Arg		
155	160	165
His Leu His Thr His Phe Gly Ala Asp Tyr Asp Trp Phe Phe Ile		
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg Leu Ala Ala Leu		
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp Leu Tyr Leu Gly Arg Ala		
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg Tyr Cys His Gly		
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser Leu Leu Leu Arg Leu Arg		
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp Ile Leu Ser Ala Arg Pro		
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser Leu Gly Val Gly		
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser Phe Glu Leu		
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser Ser Ala Phe Leu		
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser Glu Gly Thr Leu Met Tyr		
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu Glu Arg Ala Tyr		
320	325	330
Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile Arg Asn Leu Thr Val		
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp Pro Val Gly Leu		
350	355	360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp  
                   365                  370                  375  
  
 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala  
                   380                  385                  390  
  
 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp  
                   395                  400                  405  
  
 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro  
                   410                  415                  420  
  
 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg  
                   425                  430                  435  
  
 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu  
                   440                  445                  450  
  
 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg  
                   455                  460                  465  
  
 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met  
                   470                  475                  480  
  
 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu  
                   485                  490                  495  
  
 Leu Val Ala Glu Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe  
                   500                  505                  510  
  
 Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu  
                   515                  520                  525  
  
 Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp  
                   530                  535                  540  
  
 Pro Phe Leu Gly Val Lys Ala Ala Ala Glu Leu Glu Arg Arg  
                   545                  550                  555  
  
 Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala  
                   560                  565                  570  
  
 Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro  
                   575                  580                  585  
  
 Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly  
                   590                  595                  600  
  
 Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp  
                   605                  610                  615  
  
 Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu  
                   620                  625                  630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
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 755 760 765  
 Gln Glu Gln Ala Asn Ser Thr  
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 cttttgaag ggtgtatgc ttggaagcat tttctgtgct ttgatcacta 150  
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
 ttgtaaaacc caaagatgtg agtcttggg ctgcagtaaa ggagacttgg 350  
 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

gttttagtca attaatatgg acacaaatga catgtggta atgatgagaa 450  
 aagcttacaa atacgcctt gataagtata gagaccaata caactggtc 500  
 ttccttgcac gccccactac gtttgctatc attgaaaacc taaagtattt 550  
 tttgttaaaa aaggatccat cacagcctt ctatctaggc cacactataa 600  
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700  
 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
 cagtttgcct gaaatatgct ggagtatttgc cagaaaatgc agaagatgct 800  
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 tggctgttac ttttatgga ctgactccaa atcagatgca tgtgatgatg 950  
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 gtaactacat atccaataaca gctgtatgtt tcttttctt ttctaatttgc 1150  
 gtggcaactgg tataaccaca cattaaagtc agtagtacat ttttaatga 1200  
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 tttgctgatt ggttaaaaaaa ttttaacagg tcttttagcgt tctaagatata 1400  
 gcaaataatgata tctctagttg tgaatttgcgt attaaagtaa aacttttagc 1450  
 tgtgtgttcc cttaacttct aatactgatt tatgttctaa gcctccccaa 1500  
 gttccaaatgg atttgccttc tcaaaaatgta caactaagca actaaagaaa 1550  
 attaaagtga aagttgaaaaa at 1572

<210> 341  
 <211> 318  
 <212> PRT  
 <213> Homo Sapien

&lt;400&gt; 341

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Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile
		20							25					30
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
		35							40					45
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
		50							55					60
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
		65							70					75
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
		80							85					90
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
		95							100					105
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
		110							115					120
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
		125							130					135
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
		140							145					150
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
		155							160					165
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
		170							175					180
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
		185							190					195
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
		200							205					210
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
		215							220					225
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
		230							235					240
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
		245							250					255
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys

260                    265                    270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln  
275                    280                    285

Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly  
290                    295                    300

His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser  
305                    310                    315

Asp Asn Asp

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<210> 343  
<211> 18  
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<400> 343  
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<210> 344  
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<210> 345  
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<210> 346  
<211> 25  
<212> DNA  
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<210> 347  
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<223> Synthetic Oligonucleotide Probe

<400> 347  
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<210> 348  
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<212> DNA  
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<220>

<223> Synthetic Oligonucleotide Probe

<400> 348  
ggattctaat acgactcact atagggctca gaaaagcgca acagagaa 48

<210> 349  
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<212> DNA  
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<220>

<223> Synthetic Oligonucleotide Probe

<400> 349  
ctatcaaatt aaccctcact aaaggatgt cttccatgcc aaccttc 47

<210> 350  
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<223> Synthetic Oligonucleotide Probe  
  
<400> 351  
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<212> DNA  
<213> Artificial Sequence  
  
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<211> 48  
<212> DNA  
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<220>  
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<210> 355  
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<212> DNA  
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<210> 356  
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<212> DNA  
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<400> 356  
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<210> 357  
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<220>  
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<400> 357  
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<210> 358  
<211> 47  
<212> DNA  
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<220>  
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<400> 358  
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<210> 359  
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<212> DNA  
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<220>  
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<400> 359  
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<210> 360  
<211> 48  
<212> DNA  
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<220>  
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<400> 360  
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<210> 361  
<211> 48  
<212> DNA  
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<220>  
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<400> 361  
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<210> 362  
<211> 47  
<212> DNA  
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<400> 362  
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<210> 363  
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<400> 363  
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<210> 364  
<211> 47  
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<220>  
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<400> 364

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<210> 365  
<211> 48  
<212> DNA  
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<211> 47  
  
<212> DNA  
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<220>  
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<210> 368  
<211> 47  
<212> DNA  
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<220>  
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<210> 369  
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<212> DNA  
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<210> 370  
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<220>

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<400> 370  
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<210> 371  
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<400> 372  
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<210> 373  
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<400> 373  
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<220>  
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<210> 376  
<211> 997  
<212> DNA  
<213> Homo Sapien  
  
<400> 376  
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&lt;210&gt; 377

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Homo Sapien

&lt;400&gt; 377

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Ile Leu Phe Leu Ser Ala Cys Phe Ile Thr Arg Cys Val Val Thr														
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Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro														
50 55 60														
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65 70 75														
Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser														
80 85 90														
Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu														
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140 145 150														
Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp														
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Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val			
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Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly			
155	160		165
His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu			
170	175		180
Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe			
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His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His  
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Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala  
215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu  
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Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly  
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Asp Phe Arg His Lys Ser Ser Phe Val Ile  
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